	Ltd.
5.1.6	Compugen
version	- 2005
GenCore	(c) 1993
	Copyright

OM protein - protein search, using sw model

August 3, 2005, 21:41:13 ; Search time 165 Seconds Run on:

(without alignments) 731.329 Million cell updates/sec

1 MANNDAVLKRLEQKGAEADQ......FEVKGKGVCRAQTMSNSGIK 312 US-10-623-567A-1 1573 Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Sequence:

2105692 segs, 386760381 residues · Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

genesequ1980s:\* genesequ2000s:\* genesequ200s:\* genesequ2001s:\* genesequ2003s:\* genesequ2003s:\* genesequ2003s:\* A\_Geneseq\_16Dec04:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		•			SUMMARIES	
Result	th.	* Query			•	
NO	. Score	Match	Length	DB	ID	Description
1	1 1573	100.0	312	. 2	ABB07442	Abb07442 Human p43
	2 1573	٦	312	9	AA029575	Aao29575 Human Pc2
	3 1573		312	_	ADH74487	Adh74487 Human wou
	4 1573	100.0	312	œ	ADP85653	Adp85653 Human end
	5 1573	_	328	4	AAB63244	Aab63244 Human bre
	6 1343	85.4	310	7	AAR72577	Aar72577 Mouse EMA
	7 831		166	ø	ABU10452	Abul0452 Immunolog
•	8 831	52.8	166	œ	ADS80906	Ads80906 Mammalian
	9 823		166		AAW14561	_
7	10 709		147	_	ABU10250	Abul0250 Immunolog
-	11 709		147	<b>c</b> 0	ADS80904	_
	2 671	42.7	294	4	ABB59210	_
	13 522.5		280	7	ABM74361	Abm74361 DNA clone
1		33.2	289	7	ABM73655	Abm73655 DNA clone
-				9	ABU10451	Abul0451 Immunolog
-	6 516	32.8	108	œ	ADS80905	Ads80905 Mammalian
7	7 510.5			'n	AAE19811	
7	8 507			_	ADN99968	_
۲				œ	ADN73157	Adn73157 Thale cre
8	0 451			-	AAB47611	Aab47611 Human ful
7			536	'n	AAE13487	Aae13487 Human tyr
7			536		ABU72380	Нишап
~	23 450	28.6	528	7	ADF76697	
7		7	528	80	ADN05830	Antipa
7	5 450	28.6	528	8	ADQ65849	Adq65849 Novel hum

10/623567 Seg. 13 Lee

	PRO polyp	_	_	Human pro	Human 1	Human Tyr	Нишап	Human end	_			Arabidops	_	_		Novel hum		Acinetoba	Protein e	
Abm80058	Adp24469	Abu64299	Aaw53962	Ade76967	Aab47613	Aae13489	Abu72382	Aaw06596	Aay69674	Aag31613	Aag31612	Aag31611	Abb60745	Abm74280	Aag08528	Adn99487	Abu72393	Ada33478	Abu16644	
ABM80058	ADP24469	ABU64299	AAW53962	ADE76967	AAB47613	AAE13489	ABU72382	AAW06596	AAY69674	AAG31613	AAG31612	AAG31611	ABB60745	ABM74280	AAG08528	ADN99487	ABU72393	ADA33478	ABU16644	
œ	8	7	N	œ	4	Ŋ	9	N	ო	m	m	m	4	7	m	8	φ	φ	9	
528	528	527	301	301	178	178	178	168	168	382	389	440	525.	265	273	123	28	720	069	
28.6	28.6	28.6	28.0	28.0	27.4	27.4	27.4	27.3	27.3	25.5	25.5	25.5	25.1	24.9	21.8	18.7	18.6	14.4	14.3	
450	450	449.5	440.5	440.5	430.5	430.5	430.5	429.5	429.5	400.5	400.5	400.5	395	391.5	343	294	293	227	225	
26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

# ALIGNMENTS

RESULT 1

Human; p43; cytostatic; anti-tumour; anti-angiogenic; EMAP II; cytokine; chemotaxis. 140. .142 /note= "betall strand" 147. .312 /note= "C-terminal domain" 1. .146
/note= "N-terminal domain" /note= "alpha 2 helix" 124. .130 /note=."alpha 3 helix" 132. .134 'note= "betal0 strand" 75. .77 /note= "beta6i strand" 79. .85 /note= "beta7 strand" 33. .56 'note= "alpha 1 helix" 70. .72 'note= "beta5i strand" /note= "beta9 strand" [19. .123 59. .66 /note= "beta4 strand" note= "beta8 strand" /nocc-10. .21 'note= "betal strand" 40. .46 /note= "beta3 strand" 28. .34 /note= "beta2 strand" Location/Qualifiers ABB07442 standard; protein; 312 AA. 23-APR-2002 (first entry) .106 Human p43 polypeptide. Homo sapiens ABB07442; Key Domain Region Domain Region Region Region **ABB07442** 

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07-NOV-2001; 2001US-0331041P.
07-NOV-2001; 2001US-0331042P.
18-DEC-2001; 2001US-0340251P.
07-JAN-2002; 2002US-0344791P.
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N-PSDB; AAL60070.
Human Pc240 protein.
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                                                                                                                                WO2003040331-A2
                                                                                                  Homo sapiens
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100.0%; Pred. No. 1.6e-135;
iive 0; Mismatches 0;
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                                                                                   14-JUN-2000; 2000WO-KR000630
                                                                                                                 14-JUN-2000; 2000WO-KR000630
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Best Local Similarity 100.
Matches 312; Conservative
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                                                                                                                                                                                 Ko Y, Kim YS,
                                                                                                                                                                                                                  WPI; 2002-098017/13.
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                  WO200195927-A1
                                                  20-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New polynucleotide for diagnosing, staging, monitoring, prognosticating, preventing or treating, or determining the predisposition to, diseases or conditions such as prostate cancer, and for research or forensic science.
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Human; differentially regulated protein; prevention; therapy; vaccine; prostate cancer; endothelial monocyte activating polypeptide II; gene therapy; Pc240.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kovacs KF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ORIG-) ORIGENE TECHNOLOGIES INC.
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RESULT

(first entry)

27-AUG-2003

AA029575;

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181 VGEIAPRTVVSGLVNHVPLEQMQNRMVILLCNLKPAKMRGVLSQAMVMCASSPEKIEILA 240
                                             The present invention relates to a compounds, compositions and methods for modulating the expression of endothelial monocyte-activating polypeptide-II (EMAP-II). EMAP-II is also known as EMAP-2, small inducible cytokine subfamily E, member 1 (SCYEI). The compound comprises antisense oligonucleotides targetted to EMAP-II. The invention is useful for preparing a composition for treating hyperproliferative disorder e.g. cancer. It is also useful in gene therapy. The present sequence is human endothelial monocyte-activating polypeptide-II (EMAP-II). This sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New oligonucleotide compound that inhibits expression of EMAP-II, useful for preparing a composition for treating hyperproliferative disorder,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMAP-II; endothelial monocyte-activating polypeptide-II; EMAP-2; SCYEI; small inducible cytokine subfamily E member 1; hyperproliferative disorder; cancer; gene therapy; human.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human endothelial monocyte-activating polypeptide-II (EMAP-II)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 22-23; 35pp; English.
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100.0%; ...
                                                                                                                                                                                                                                                                                                                 ADP85653 standard; protein; 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dobie KW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-DEC-2002; 2002US-00316232.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-DEC-2002; 2002US-00316232
                                                                                                                                                 CRAQTMSNSGIK 312
                                                                                                                                                                                           301 CRAQTMSNSGIK 312
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Matches 312; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     is used in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dean NM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2004-440333/41.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; ADP85584.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 312 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US2004110144-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                  26-AUG-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bennett CF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-JUN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             e.g. cancer
                                                                                                                                                                                                                                                                                                                                                                   ADP85653;
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                                                                                                                                              301
                                                                                                                                                                                                                                                                                                  ADP85653
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to the use of one or more polypeptides (I) chosen from a polypeptide having a fully defined p43 sequence of 312 amino acids as given in the specification and a polypeptide having 70% or more sequence homology with (S1), for the manufacture of the pharmaceutical composition (II) which is intended to stimulate wound healing in a subject. The plolypeptide of the invention is useful for the manufacture of the pharmaceutical composition (II) which is intended to stimulate wound healing in a subject. The wound is chosen from burn, ulcer, trauma, post-surgical, post-child birth, chronic wound and dermatities. The burn is chosen from sun burn, chemical burn, radiation burn, and thermal burn. The ulcer is chosen from pressure ulcer, plaster ulcer and decubitus ulcer. The chronic wound is chosen from bedsores, pressure sores, clicar the chronic wound is chosen from bedsores, pressure sores. Climabetes-related and poor circulation-related. The dermatitis is chosen from impeting, intertiigo, follicultiis and ecasma. The current sequence from impeting, intertiigo stimulating polypeptide of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              p43 polypeptide, for the manufacture of pharmaceutical composition of to stimulate wound healing in a subject.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 ELKQELIQAEIQNGVKQIAFPSGTPLHANSMVSENVIQSTAVTTVSSGTKEQIKGGTGDE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 KKAKEKIEKKGEKKEKKQOSIAGSADSKPIDVSRLDLRIGCIITARKHPDADSLYVEEVD 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MANNDAVLKRLEGKGAEADQIIEYLKQQVSLLKEKAILQATLREEKKLRVENAKLKKEIE 60
                                                                                                                                                                                                                    Vulnerary; antiulcer; dermatological; antiallergic; antiinflammatory; wound healing; burn; ulcer; trauma; post-surgical; post-child birth; chronic wound; dermatitis; sunburn; chemical burn; radiation burn; thermal burn; pressure ulcer; plaster ulcer; decubitus ulcer; bedsores; pressure sore; diabetes; poor circulation; impetigo; intertrigo; folliculitis; eczema; p43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MANNDAVLKRLEQKGAEADQIIEYLKQQVSLLKEKAILQATLREEKKLRVENAKLKKEIE
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                                                                                                                                                                          Human wound healing stimulating polypeptide p43, SEQ ID 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 1573; DB 8;
100.0%; Pred. No. 1.6e-135;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 1; 20pp; English
                                ADH74487 standard; protein; 312 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-JUL-2003; 2003EP-00016724.
                                                                                                                             (first entry)
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Matches 312; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                              EP1384486-A1
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A mouse methA sarcoma cDNA library was screened with a probe based on the N-terminal sequence of mouse EMAPII. Overlapping clones were combined to obtain a contiguous full-length sequence (given in AAQ86718) encoding a 33 kDa protein (AAR72577). Recombinant EMAPII was expressed in E. coli. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New endothelial monocyte activating polypeptide II - induces chemotaxis, inflammation and tissue factor, useful for treating tumours, also related antibodies, DNA and active fragments.
                                  ELKQELIQAEIQNGVKQIAFPSGTPLHANSMVSENVIQSTAVTTVSSGTKEQIKGGTGDE
                                                                                               KKAKEKI EKKGEKKEKKOOSIAGSADSKPIDVSRLDLRIGCIITARKHPDADSLYVEEVD
                                                                                                                                                          1 MANNDAVLKRLEQKGAEADQIIEYLKQQVSLLKEKAILQATLREEKKLRVENAKLKKEIE
                                                                             KKAKEKIEKKGEKKEKKQQSIAGSADSKPIDVSRLDLRIGCIITARKHPDADSLYVEEVD
                                                                                                                                        VGBIAPRIVVSGLVNHVPLEQMQNRMVILLCNLKPAKMRGVLSQAMVMCASSPEKIEILA
                                                                                                                                                                                                    PPNGSVPGDRITFDAFFGEPDKELNPKKKIWEQIQPDLHTNDECVATYKGVPFEVKGKGV
                                                                                                                                                                                                                   PPNGSVPGDRITFDAFPGEPDKELNPKKKIWEQIQPDLHTNDECVATYKGVPFEVKGKGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMAPII; endothelial monocyte activating polypeptide II; chemotaxis; inflammation; tissue factor; tumor; cancer; therapy; methA; sarcoma.
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llarity 85.9%; Pred. No. 2e-114;
Conservative 13; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kayton M, Libutti SK;
                                                                                                                                                                                                                                                                                                                                                                        AAR72577 standard; protein; 310 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 4; 180pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                       CRAQTMSNSGIK 328
                                                                                                                                                                                                                                                               CRAQIMSNSGIK 312
                                                                                                                                                                                                                                                                                                                                                                                                                                   (revised)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1995-147389/19.
N-PSDB; AAQ86718.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse EMAPII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
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Best Local Simi:
Matches 269;
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29-SEP-1995
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                                                                 VGEIAPRIVVSGLVNHVPLEQMQNRMVILLCNLKPAKMRGVLSQAMVMCASSPEKIEILA 240
VGEIAPRIVVSGLVNHVPLEQMQNRMVILLCNLKPAKMRGVLSQAMVMCASSPEKIEILA 240
                                                                                                            PPNGSVPGDRITFDAFPGEPDKELNPKKKIWEQIQPDLHTNDECVATYKGVPFEVKGKGV 300
                                                                                                                             241 PPNGSVPGDRITFDAFPGEPDKELNPKKKIWEQIQPDLHTNDECVATYKGVPFEVKGKGV 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16
                                                                                                                                                                                                                                                                                                                                                                        Human breast cancer associated antigen protein sequence SEQ ID NO:606.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MANNDAVLKRLEQKGAEADQIIEYLKQQVSLLKEKAILQATLREEKKLRVENAKLKKEIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acids encoding breast, gastric and prostate cancer associated antigen precursors, useful for diagnosing and treating a condition characterized by expression of an abnormal amount of a protein, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MANNDAVLKRLEQKGAEADQIIEYLKQQVSLLKEKAILQATLREEKKLRVENAKLKKEIE
                                                                                                                                                                                                                                                                                                                                                                                                     Human, breast cancer, gastric cancer, prostate cancer, diagnosis,
cancer associated antigen, cytostatic, cancer vaccine.
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100.0%; Pred. No. 1.7e-135;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; Page 478; 799pp; English.
                                                                                                                                                                                                                                                                               AAB63244 standard; protein; 328 AA.
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99US-0153454P.
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                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                      CRAQTMSNSGIK 312
                                                                                                                                                                                                    CRAQTMSNSGIK 312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
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10-SEP-1999;
                                                                                                                                                                                                                                                                                                                                          26-MAR-2001
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Matches 312;
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(KIMS/) (KOYY/) Kim S,

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The present invention relates to a method of enhancing an immune response. The method involves administering an immunological enchancement agent having the N-terminal domain of p43 protein to a cell or tissue. The invention is useful for enhancing an immune response with an immunological enhancement agent in apoptotic disorders such as cancer. The present sequence is the mammalian p43(91-256) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DVSRLDLRIGCIITARKHPDADSLYVEEVDVGEIAPRTVVSGLVNHVPLEQMQNRMVILL 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DVSRLDLRIGCIITARKHPDADSLYVEEVDVGEIAPRTVVSGLVNHVPLEQMQNRMVILL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MVSENVIQSTAVTTVSSGTKEQIKGGTGDEKKAKEKIEKKGEKKEKKQQSIAGSADSKPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Enhancing an immune response using an immunological enhancement agen'
having the N-terminal domain of the p43 protein, useful in apoptotic
                                                                                                                                                                                                                                                                                                                                                                      disorder; cancer; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     211 CNLKPAKMRGVLSQAMVMCASSPEKIEILAPPNGSVPGDRITFDAF 256
                                                                                                                                       CNLKPAKMRGVLSQAMVMCASSPEKIEILAPPNGSVPGDRITFDAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 831; DB 8; I
Pred. No. 7.8e-68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 3; 12pp; English.
                                                                                                                                                                                                                                                                                                                                                                           Immune response; p43; apoptotic di
immunostimulant; cytokine-agonist.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52.00
100.08; Fig.
                                                                                                                                                                                                                                          ADS80906 standard; protein; 166
                                                                                                                                                                                                                                                                                                                                            Mammalian p43(91-256) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-APR-2004; 2004US-00823730.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-JUN-2001; 2001KR-00031310.
16-AUG-2001; 2001US-00930169.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52.8%;
                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   disorders such as cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 166; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (IMAG-) IMAGENE CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2004-689153/67.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 166 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             US2004185060-A1
                                                                                                                                                                                                                                                                                                         16-DEC-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-SEP-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                        ADS80906;
                                                       151
                                                                                      61
                                                                                                                                                       121
                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kim
                                                                                                                                                                                                                                          셤
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                                      ELKOELIQAEIQNGVKQIAFPSGTPLHANSMVSENVIQSTAV-TTVSSGTKEQIKGGTGD 119
                                                                                                                           APPNGSVPGDRITFDAFPGEPDKELNPKKKIWEQIQPDLHTNDECVATYKGVPFEVKGKG 299
                                                                                                                                                                                                                                                                           297
                                                                                                          EKKAKEKIEKKGEKKEKKQQSIAGSADSKPIDVSRLDLRIGCIITARKHPDADSLYVEEV 179
        MATNDAVLKRLEQKGAEADQIIEYLKQQVALLKEKAILQATMREEKKLRVENAKLKKEIE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New immunological enhancement agent comprising an N-terminal peptide of p43, useful for increasing the amount of tumor necrosis factor and interleukin-8 to improve the immune response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence represents an immunological enhancement agent comprising an N-terminal peptide of p43. The peptide can act as a cytokine to increase the amount of tumour necrosis factor (TNF) and interleukin-8 useful for improving an immune response and used as an immunological enhancement agent. The present sequence represents the amino acid sequence of the immunological enhancement 390t.
                                                           DVGEIAPRTVVSGLVNHVPLEQMQNRMVILLCNLKPAKMRGVLSQAMVMCASSPEKIEIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                agonist; p43; cytokine; interleukin-8; TNF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52.8%; Score 831; DB 6; Length 166; 100.0%; Pred. No. 7.8e-68; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Immunological enhancement agent p43 (91-256).
                                                                                                                                                                                                                                                                                                                                                                                                                                 ABU10452 standard; protein; 166 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 3; Page 5; 12pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-AUG-2001; 2001US-00930169.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-JUN-2001; 2001KR-00031310
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VCRAQTMANSGIK 310
                                                                                                                                                                                                                                                                                                              VCRAQTMSNSGIK 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Immunostimulant; cytokine tumour necrosis factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 100.
Matches 166; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-447359/42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 166 AA;
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KO Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ko Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-AUG-2003
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Gaps

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Length 166; Indels 150

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91 MVSENVIQSTAVTTVSSGTKEQIKGGTGDEKKAKEKIEKKGEKKEKKQQSIAGSADSKPI 150

Query Match Best Local S

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                                                                                                                                                                                                                                                                                                                                                                                                                                                (KOYY/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kim S,
                                                                                                                     RESULT 10
                                                                                                                                                            셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   involves subcutaneous, intraperitoneal, intravenous, intracranial or involves subcutaneous, intraperitoneal, intravenous, intracranial or intractumoural administration of an endothelial monocyte activating polypeptide II (EMAP-II), or a EMAP-II-derived polypeptide. The present sequence represents murine EMAP-II which can be used to produce the EMAP-II derived polypeptide as long as it contains at least ninety percent inderived polypeptide as long as it contains at least ninety percent carcinoma (administered intraperitoneally) or gliobiascoma (administered intraperitoneally) or gliobiascoma (administered intraperitoneally) or gliobiascoma (administered intrateumourally by positive pressure microinfusion). Inhibition of engliogenesis to treatment of eye diseases associated with excessive blood vessel formation, especially retinopathy (diabetic, related to sickle cell anaemia, retinopathy of prematurity or age-related macular degeneration). Intraperitoneal administration allows tumours too small (not over 2 mm in diameter) for intratumoural injection to be
                                                                                                                                       EMAP-II; inhibitor; endothelial cell formation; blood vessel; retinopathy; tumour; subcutaneous; intraperitoneal; intravenous; intracranial; intratumoural; carcinoma; glioblastoma; pessitive pressure microinfusion; aortic cell; angiogenesis; eye disease; diabetes; sickle cell anaemia; prematurity; age-related macular degeneration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Treatment of tumours with endothelial monocyte activating peptide II - also used to inhibit growth of endothelial cells and formation of blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 52.3%; Score 823; DB 2; Length 166; Best Local Similarity 93.9%; Pred. No. 4.2e-67; Matches 155; Conservative 5; Mismatches 5; Indel8
                                                                                                                     Endothelial monocyte activating polypeptide II.
                                                                                                                                                                                                                                                                                                label= Ser, Met, Gly
                                                                                                                                                                                                                                                                       Location/Qualifiers
                                       AAW14561 standard; protein; 166 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 13; Page 73; 104pp; English
                                                                                                                                                                                                                                                                                                                        /label= Cys, Arg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              treated before they grow larger
                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UYCO ) UNIV COLUMBIA NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       vessels, e.g. in retinopathy.
                                                                                                                                                                                                                                                                                                                                                                                                                                    95US-0003898P.
                                                                                                                                                                                                                                                                                                                                                                                                         96WO-US015007
                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schwarz M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1997-202617/18.
                                                                                                                                                                                                                                                                                                             Misc-difference 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 166 AA;
                                                                                                                                                                                                                                                                                  Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                         18-SEP-1996;
                                                                                                                                                                                                                                            Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                    18-SEP-1995;
                                                                                            01-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                27-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Stern D,
                                                                 AAW14561;
            RESULT 9
                            AAW14561
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MANNDAVLKRLEQKGAEADQIIEYLKQQVSLLKEKAILQATLREEKKLRVENAKLKKEIE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New immunological enhancement agent comprising an N-terminal peptide of p43, useful for increasing the amount of tumor necrosis factor and interleukin-8 to improve the immune response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence represents an immunological enhancement agent comprising an N-terminal peptide of p43. The peptide can act as a cytokine to increase the amount of tumour necrosis factor (TNF) and interleukin-8 useful for improving an immune response and used as an immunological enhancement agent. The present sequence represents the amino acid sequence of the immunological enhancement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MANNDAVLKRIEGKGABADQIIEYIKQQVSLLKEKAILQATLREEKKLRVENAKLKKEIE
                                                                                                                                                                                                                                                                                                                                                                                                     Immunostimulant; cytokine agonist; p43; cytokine; interleukin-8; TNF; tumour necrosis factor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 147;
                                                                  KKIWEQIQPDLHTNDECVATYKGVPFEVKGKGVCRAQTMSNSGIK 312
                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45.1%; Score 709; DB 6; Lv
100.0%; Pred. No. 1e-56;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                 Immunological enhancement agent p43 (1-147)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KKAKEKIEKKGEKKEKKQQSIAGSADS 147
                                                                                                                                                                                                                            Ā.
                                                                                                                                                                                                                              ABU10250 standard; protein; 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-JUN-2001; 2001KR-00031310
                                                                                                                                                                                                                                                                                                                    (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.
Matches 147; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 147 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US2003004309-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (KIMS/) KIM S. (KOYY/) KO Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ko Y;
                                                                                                                                                                                                                                                                                                                      01-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-JAN-2003
                                                                  268
                                                                                                             122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
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RESULT 11

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148 KPIDVSRLDLRIGCIITARKHPDADSLYVEEVDVGEIAPRTVVSGLVNHVPLEQMQNRMV 207

KPIDASRLDLRIGXIVTAKKHPDADSLYVEEVDVGEAAPRTVVSGLVNHVPLEQMQNRMV

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ADS80904

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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA sequence data for this patent did not form part of printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LIQAEIQNGVKQIAFP-----SGTPLHANSMVSENVIQSTAVTTVSSGTKEQIKGGTG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEKKAKEKIEKKGEKKEKKQQSIAGSADSKPIDVSRLDLRIGCIITARKHPDADSLYVEE 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              179 VDVGEIAPRTVVSGLVNHVPLEQMQNRMVILLCNLKPAKMRGVLSQAMVMCASSPEKIEI 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LAPPNGSVPGDRITFDAFPGBPDKELNPKKKIWEQIQPDLHTNDECVATYKGVPFBVKGK 298
                                                                                                                                                                                                                                                                                                                                New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 ADLQQIASNNERAEALINSIEAEISGIQQ----QLVERQKQELIKENAALAKEVEAALAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 AVLKRLEQKGAEADQIIEYLKQQVSLLKEKAILQATLREEKKLRVENAKLKKEIEELKQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 4422; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42.7%; Score 671; DB 4;
44.9%; Pred. No. 8.6e-53;
ative 57; Mismatches 88.
                                                                                                                                                                                                                                        Myers EW;
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                                                                                                                                                                                                                                          PWD,
                                                                                                          23-MAR-2001; 2001WO-US009231
                                                                                                                                               23-MAR-2000; 2000US-0191637P
11-JUL-2000; 2000US-00614150
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Drosophila melanogaster.
                                                                                                                                                                                                                                          Adams M,
                                                                                                                                                                                                                                                                               WPI; 2001-656860/75
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                                                                                                                                                                                                     (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                  N-PSDB; ABL03313
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                                  WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                            interactions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Simi
                                                                                                                                                                                                                                        Venter JC,
                                                                       27-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ELKQELIQAEIQNGVKQIAFPSGTPLHANSMVSENVIQSTAVTTVSSGTKEQIKGGTGDE 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MANNDAVLKRLEOKGAEADOIIEYLKOOVSLLKEKAILOATLREEKKLRVENAKLKKEIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Enhancing an immune response using an immunological enhancement agent having the N-terminal domain of the p43 protein, useful in apoptotic disorders such as cancer.
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                                                                                                                                               Immune response; p43; apoptotic disorder; cancer; cytostatic;
immunostimulant; cytokine-agonist.
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100.0%; Pred. No. 1e-56;
ive 0; Mismatches 0; Indels
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   ADS80904 standard; protein; 147
                                                                                                                                                                                                                                                                                                                                                         05-JUN-2001; 2001KR-00031310.
16-AUG-2001; 2001US-00930169.
                                                                                                              Mammalian p43(1-147) protein.
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Best Local Similarity 100.
Matches 147; Conservative
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                                        ADS80904
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Kim S,

65 57

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Length 294; 88; Indels 280

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17-OCT-2003 (first entry)
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                                                                                                                                                                                                                                                                                                                                                           The present invention relates to oligonucleotide clones originating in barley (Hordeum vulgare) which contain single nucleotide polymorphisms (SNP). The oligonucleotides may be used for analysis of SNPs among barley varieties, identification of particular varieties and genotype-phenotype analysis, isolation of specific genes and creation of new varieties by transformation of barley varieties with them and production of new barley varieties with desired properties. The present sequence represents an oligonucleotide clone sequence featured in the specification. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KQQSIAGSADSKPIDVSRLDLRIGCIITARKHPDADSLYVEEVDVGEIAPRTVVSGLVNH 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           197 VPLEQMQNRMVILLCNLKPAKMRGVLSQAMVMCASSPE--KIEILAPPNGSVPGDRITFD 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Barley; single nucleotide polymorphism; SNP; genotype-phenotype analysis.
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barley
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           ONA clone originating in barley containing SNP sequence #771.
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                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID XX; 284pp; Japanese.
                                                                                                                                              20-DEC-2001; 2001JP-00387059.
20-DEC-2001; 2001JP-00387131.
20-DEC-2001; 2001JP-00403299.
20-DEC-2001; 2001JP-00403309.
27-SEP-2002; 2002JP-00327515.
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                                                                                                                         2002WO-IB005403
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108; Conserva
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                                                                             WO2003057877-A1:
                                                       Hordeum vulgare
                                                                                                                                                                                                                                                                                                                     characteristics
                                                                                                                         16-DEC-2002;
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Best Local &
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ABM73655 standard; protein; 289

ABM73655;

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                                                       Barley; single nucleotide polymorphism; SNP; genotype-phenotype analysis.
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barley
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Single nucleotide polymorphism sites in barley varieties and I sequences containing them for analysis and identification of twarieties and production of barley transformants with desired characteristics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 289;
DNA clone originating in barley containing SNP sequence #65.
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45.4%; Pred. No. 3.5e-39;
iive 42; Mismatches 77;
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                                                                                                                                                                                                                                                                                                                                                                                    2001JP-00387131.
2001JP-00403299.
2001JP-00403300.
2002JP-00327515.
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Matches 108; Conservative
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                                                                                                                     Hordeum vulgare
                                                                                                                                                                          WO2003057877-A1
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20-DEC-2001;
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New immunological enhancement agent comprising an N-terminal peptide of p43, useful for increasing the amount of tumor necrosis factor and interleukin-8 to improve the immune response.
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                                                                  Immunostimulant; cytokine agonist; p43; cytokine; interleukin-8; TNF; tumour necrosis factor.
                                          Immunological enhancement agent p43 (1-108).
                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 2; Page 5; 12pp; English
                                                                                                                                                                                                     16-AUG-2001; 2001US-00930169
                                                                                                                                                                                                                                 05-JUN-2001; 2001KR-00031310.
               (first entry)
                                                                                                                                                                                                                                                                                                                                    WPI; 2003-447359/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 108 AA;
                                                                                                                                             US2003004309-A1.
                                                                                                                                                                                                                                                            (KIMS/) KIM S. (KOYY/) KO Y.
                                                                                                                                                                                                                                                                                                        Ko Y;
                                                                                                                                                                         02-JAN-2003.
               01-AUG-2003
                                                                                                                Mammalia.
                                                                                                                                                                                                                                                                                                        Kim S,
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Query Match 32.8%; Score 516; DB 6; Length 108; Best Local Similarity 100.0%; Pred. No. 3.4e-39; Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps

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152.5.5
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Sequence 36, Appl
Sequence 3, Appli
Sequence 35, Appl
Sequence 35, Appl
Sequence 35, Appl
Sequence 11, Appli
Sequence 11, Appli
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1, Appli
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132, App
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6201, Ap
4, Appli
10686, A
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10567, A
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554.536 Million cell updates/sec
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                                                                                                                                                   US-10-623-567A-1 .
1573
1 MANNDAVLKRLEQKGAEADQ.......FEVKGKGVCRAQTMSNSGIK 312
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                                                                                          August 3, 2005, 21:47:49 ; Search time 42 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                   1: /cgn2 6/prodata/1/iaa/5A_COMB.pep:*
2: /cgn2 6/prodata/1/iaa/5B_COMB.pep:*
3: /cgn2 6/prodata/1/iaa/6A_COMB.pep:*
4: /cgn2 6/prodata/1/iaa/6B_COMB.pep:*
5: /cgn2 6/prodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2 6/prodata/1/iaa/PCTUS_COMB.pep:*
              GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-851-026-36
US-09-9456A-36
US-08-129-456A-36
US-08-129-456A-36
US-09-129-456A-36
US-09-129-456A-36
US-09-129-456A-17
US-08-129-456A-11
US-08-129-456A-11
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                                                                                                                                                                                                                                                     513545 segs, 74649064 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                     OM protein - protein search, using sw model
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Maximum DB seq length: 200000000
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Match Length DB
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1510
1343
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1343
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                                                                                                                                                                                                            Scoring table:
                                                                                                                                                                                  Sequence:
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Result

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APPLICANT: Stern, David M.
APPLICANT: Clauss, Matthias
APPLICANT: Kao, Jane
APPLICANT: Kayton, Mark
APPLICANT: Libutti, Steven K
APPLICANT: Libutti, Steven K
TITLE OF INVENTION: Endothelial Monocyte Activating
TITLE OF INVENTION: Polypeptide II: A Mediator Which Activates Host Response
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham, LLP
Sequence 2, Appli
Sequence 2751, Ap
Sequence 21554, Ap
Sequence 21654, Ap
Sequence 21656, Ap
Sequence 3507, Ap
Sequence 4, Appli
Sequence 7643, Ap
Sequence 7643, Ap
Sequence 19, Appli
Sequence 19, Appli
Sequence 11535, A
Sequence 11535, A
Sequence 11535, A
Sequence 6566, Appli
Sequence 11535, A
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99.7%; Score 1568; DB 3; Length 312;
Best Local Similarity 99.7%; Pred. No. 2.9e-136;
Matches 311; Conservative 0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.30, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/360,821B
FILING DATE: 08-OCT-96
CLASSIFTCATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41735-A-PCT-US
TELEPHONE: 212-278-0400
TELEPAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 312 amino acids
"TELEPAX: anino acids
"TELEPAX: anino acids
"TELEPAX: anino acids
"TELEPAX: anino acids
                                                             US-09-252-991A-21654
US-09-489-099A-8243
US-09-252-991A-17566
US-09-540-236-3507
US-08-844-059-4
US-09-431-202-4
US-09-543-681A-5403
US-09-543-681A-7643
US-09-134-078-19
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PCT-US93-03077-1
US-09-949-016-6596
US-09-949-016-10404
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                                                                                                                                                                                                                                                                                                                                                                                                                           ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 36, Application US/08360821B Patent No. 6228837 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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120

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180

300

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Sequence 7144, Application US/09949016
; Sequence 7144, Application US/09949016
; Patent No. 681239
; GENERAL INFORMATION:
; APPLICANTY VENTER, U. Craig et al.
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
; FILE REFERENCE: CLOOD.307
; CURRENT APPLICATION NUMBER: 60/241,755
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR PLILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FREEKSEQ for Windows Version 4.0
; SEQ ID NO 7144
; LENGTH: 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VGEIAPRTVVSGLVNHVPLEQMQNRMVILLCNLKPAKMRGVLSQAMVMCASSPEKIEILA 240
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                                                                                                                                                                                                                                                          9 MANNDAVLKRLEQKGAEADQIIEYLKQQVSLLKEKAILQATLREEKKLRVENAKLKKEIE
                                                                                               VGEI APRTVVSGLVNHVPLEQMQNRMVILLCNLKPAKMRGVLSQAMVMCASSPEKIEILA
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                                                                                                                                                          ELKQELIQAEIQNGVKQIAFPSGTPLHANSMVSENVIQSTAVTTVSSGTKEQIKGGTGDE
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                                        Indels
Score 1568; DB 4;
Pred. No. 2.9e-136;
0; Mismatches 1;
Query Match
Best Local Similarity 99.7%;
Matches 311; Conservative
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Best Local Similarity 99.7
Matches 311; Conservative
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US-09-949-016-7144
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Kao, Janet
Kao, Janet
Kayton, Mark
Kayton, Mark
Libutti, Steven K
Libutti, Steven K
TITLE OF INVENTION: Endothelial Monocyte Activating
Polypeptide II: A Mediator Which Activates Host Response
                                                                                                                                                                                                                                     181 VGEIAPRTVVSGLVNHVPLEQMQNRMVILLCNLKPAKORGVLSQAMVMCASSPEKIEILA 240
                                                                                   ELKQELIQAEIQNGVKQIPFPSGTPLHANSMVSENVIQSTAVTTVSSGTKEQIKGGTGDE 120
                                                                                                                                                              121 KKAKEKIEKKGEKKEKKQQSIAGSADSKPIDVSRLDLRIGCIITARKHPDADSLYVEEVD 180
                                                                                                                                                                                                                     VGEIAPRIVVSGLVNHVPLEQMONRMVILLCNLKPAKMRGVLSQAMVMCASSPEKIEILA 240
                                                                                                                                                                                                                                                                                                                     241 PPNGSVPGDRITFDAFPGEFDKELNPKKKIWEQIQPDLHTNDECVATYKGVPFEVKGKGV 300
                                                                                                                                          KKAKEKIEKKGEKKEKKQQSIAGSADSKPIDVSRLDLRIGCIITARKHPDADSLYVEEVD 180
                                                                                                                                                                                                                                                                                                PPNGSVPGDRITFDAFPGEPDKELNPKKKIWEQIQPDLHTNDECVATYKGVPFEVKGKGV 300
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOOFWARE: Patentin Release #1.30, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/851,026
FILING DATE: 07-M9-2001
CLASSIFICATION: CURNOMP
PRIOR APPLICATION DATA:
ATORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 41735-A-PCT-US
TELECOMMINICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 36:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham, Lide
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US-09-851-026-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: White, John P. REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 312 amino acida
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
CULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 36, Application US/09851026; Patent No. 6734168; GENERAL INFORMATION: APPLICANT: Stern, David M. Clause, Matthias
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                CRAQTMSNSGIK 312
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US-09-851-026-36
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61 ELKOELIQAEIONGVKOIAFPSGTPLHANSMVSENVIOSTAV-TTVSSGTKEOIKGGTGD 119
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                                                                                     240 APPNGSVPGDRITFDAFPGEPDKELNPKKKIWEQIQPDLHTNDECVATYKGVPFBVKGKG 299
178 DVGEIAPRTVVSGLVNHVPLEQMQNRMVILLCNLKPAKMRGVLSQAMVMCASSPEKIBIL 237
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                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Stern, David M.
APPLICANT: Clause, Matchias
APPLICANT: Kao, Janet
APPLICANT: Kao, Janet
APPLICANT: Kayton, Mark
APPLICANT: Libuti, Steven K.
TITLE OF INVENTION: Endothelial-Monocyte Activating
TITLE OF INVENTION: Polypeptide II: A Mediator Which
TITLE OF INVENTION: Activates Host Response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0 Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Cooper & Dunham LLP STREET: 1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                ; Sequence 36, Application US/08129456A
; Patent No. 5641867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 29-SEP-1993
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REPREBNCE/DOCKET NUMBER: 4173!
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 278 0400
TELEPHONE: 212 391 0526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-SEP-1993
                                                                                                                                                                                                          298 VCRAQTMSNSGIK 310
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Best Local Similarity 85.9
Matches 269; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper &
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STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 10036
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US-08-129-456A-36
                                                                                                                                                                                                                                                                                                                    RESULT 5
US-08-129-456A-36
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                                      PPNGSVPGDRITFDAFPGEPDKELNPKKKIWEQIQPDLHTNDECVATYKGVPFEVKGKGV 300
                                                                         PPNGSVPGDRITFDAFPGEPDKELNPKKKIWEQIQPDLHTNDECVATYKGVPFEVKGKGV 308
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                                                                                                                                                                                                                                                                                                                                                 JULEANT: Clause, Matchias
APPLICANT: Clause, Matchias
APPLICANT: Kao, Janet
APPLICANT: Kayton, Mark
APPLICANT: Libutti, Steven K.
TITLE OF INVENTION: Endothelial-Monocyte Activating
TITLE OF INVENTION: Polypeptide II: A Mediator Which
TITLE OF INVENTION: Activates Host Response
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEB: Coone-
STREF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTAX: USAN
ZIP: 10036
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0 Version #1.30
SOFTWARE: PatentIn Release #1.0 Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/129,456A
FILING DATE: 29-SEP-1993
CLASSIFFCATION: 530
ATIONEV/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 41735
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 278 0400
TELEPHAX: 212 391 0526
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
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FORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
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Patent No. 5641867
GENERAL INFORMATION:
APPLICANT: Stern, David M.
APPLICANT: Clauss, Matchias
APPLICANT: Kao, Janet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 310 amino acids
amino acid
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Matches 306; Conservative
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STATE: New York
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61 ELKQELIQAEIQNGVKQIAFPSGTPLHANSMVSENVIQSTAV-TTVSSGTKEQIKGGTGD 119
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180 DVGEIAPRTVVSGLVNHVPLEQMQNRMVILLCNLKPAKMRGVLSQAMVMCASSPEKIEIL 239
                                                                    240 APPNGSVPGDRITFDAFPGEPDKELNPKKKIWEQIQPDLHTNDECVATYKGVPFEVKGKG 299
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                                                                                                                                                                                                                                                                                                   APPLICANT: Bandman, Olga
APPLICANT: Coleman, Roger
APPLICANT: Au-Voung, Janice
APPLICANT: Murry, Lynn E.
TITLE OF INVENTION: NOVEL MONOCYTE ACTIVATING CYTOKINE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match

85.4%; Score 1343; DB 3;
Best Local Similarity 85.9%; Pred. No. 1.5e-115;
Matches 269; Conservative 13; Mismatches 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PF-0117 US
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                                                                                                                                                                                                                                                                                                                                                                                                                 LICYTE Pharmac CITY: 3174 Porter Drive CITY: Palo Alto
                                                                                                                                    300 VCRAQTMSNSGIK 312
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ZIP: 94304
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61 ELKQELIQAEIQNGVKQIAFPSGTPLHANSMVSENVIQSTAV-TTVSSGTKEQIKGGTGD 119
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85.9%; Pred. No. 1.5e-115;
ive 13; Mismatches 27; Indels
                                                                                                                                                                                                                                      APPLICANT: Bandman, Olga
APPLICANT: Coleman, Roger
APPLICANT: Au-Young, Janice
APPLICANT: Au-Young, Janice
APPLICANT: Murry, Lynn E:
TITLE OF INVENTION: NOVEL MONOCYTE ACTIVATING CYTOKINE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incvre re-
STREEN
                                                                                                                                                                                                                                                                                                                                                                           STATE: CA
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CUMPLOIRER: LED.
CUMRENT APPLICATION DATA:
CUMRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/705,868
FILING DATE: Filed Herewith
ATTONNEY, AGENT INPRORMATION:
NAME: Billings, Lucy J.
REFERENCE/DOCKET NUMBER: 96,749
REFERENCE/DOCKET NUMBER: PF-0117 US
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION SEQ. 10.0: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 310 amino acids
                                                                                                                                                                                                                 'US-08-705-868-3
; Sequence 3, Application US/08705868
; Patent No. S085798
; GENERAL INFORMATION:
APPLICANT: Bandman, Olga
; APPLICANT: COLeman, Roger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                        298 VCRAQTMANSGIK 310
                                                                                                                      VCRAQTMSNSGIK 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 85.94
Matches 269; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              u.s.
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Kao, Janet
Kayton, Mark
Kayton, Mark
Libutti, Steven K
TITLE OF INVENTION: Endothelial Monocyte Activating
Polypeptide II: A Mediator Which Activates Host Response
                                                                                                                   240 APPNGSVPGDRITFDAFPGEPDKELNPKKKIWEQIQPDLHTNDECVATYKGVPFEVKGKG 299
                                                                                                                                                                                                     DVGEIAPRTVVSGLVNHVPLEQMQNRMVILLCNLKPAKMRGVLSQAMVMCASSPEKIEIL 239
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COMPUTE: INP. TOPPY JED.

COMPUTE: INP. Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Perentin Release #1.30, Version #1.30

CURRENT APPLICATION NUMBER: US/09/851,026

FILING DATE: 07-May-2001

CLASSIPICATION: -UNknown>
PRIOR APPLICATION: -UNknown>
PRIOR APPLICATION: OUNMBER: US/08/360,821

RILING DATE: 08-COT-96

ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678

REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 41735-A-PCT-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Cooper & Dunham, LLP
STREET: 1185 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 35:
US-09-851-026-35
                                                                                                                                                                                                                                                                                                                                                                                    US-09-851-026-35
; Sequence 35, Application US/09851026
; Patent No. 6734168
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 310 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clauss, Matthias
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 212-391-0525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Stern, David M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEC ID NO: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 10036
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                         298 VCRAQTMANSGIK 310
                                                                                                                                                                                                                                                                 300 VCRAQTMSNSGIK 312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
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APPLICANT: Clauss, Matthias
APPLICANT: Clauss, Matthias
APPLICANT: Kao, Janet
APPLICANT: Kayton, Mark
APPLICANT: Libutti, Steven K
TITLE OF INVENTION: Endothelial Monocyte Activating
TITLE OF INVENTION: Polypeptide II: A Mediator Which Activates Host Response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ELKQELIQAEIQNGVKQIAFPSGTPLHANSMVSENVIQSTAV-TTVSSGTKEQIKGGTGD 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DVGEIAPRITVVSGLVNHVPLEQMQNRMVILLCNLKPAKMRGVLSQAMVMCASSPEKIEIL 239
                                                                                                    240 APPNGSVPGDRITFDAFPGEPDKELNPKKKIWEQIQPDLHTNDECVATYKGVPFEVKGKG 299
                                                                                                                                                                                        EKKAKEKIEKKGEKKEKKQQSIAGSADSKPIDVSRLDLRIGCIITARKHPDADSLYVEEV 179
                     9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.30, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/360,821B
FILING DATE: 08-OCT-96
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85.4%; Score 1343; DB 3;
85.9%; Pred. No. 1.5e-115;
iive 13; Mismatches 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3: Cooper & Dunham, LLP
1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1 20
                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 35, Application US/08360821B; Patent No. 6228837; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REPRENCE/DOCKET NUMBER: 4173
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 310 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
STREET: 11
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207 VILLCNLKPAKWRGVLSQAMVMCASSPEKIEILAPPNGSVPGDRITFDAFPGEPDKELNP 266
                                                                                                                                     RITFDAFPGEPDKELNPKKKIWEQIQPDLHTNDECVATYKGVPFEVKGKGVCRAQTMSNS 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 SKPIDASRLDLRIGGIVTAKKHPDADSLYVBEVDVGEAAPRTVVSGLVNHVPLEQMQNRM 60
                                              190 VSGLVNHVPLEQMQNRMVILLCNLKPAKMRGVLSQAMVMCASSPEKIEILAPPNGSVPGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      147 SKPIDVSRLDLRIGCIITARKHPDADSLYVEEVDVGEIAPRTVVSGLVNHVPLEQMQNRM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 166;
                                                                                                                                                                                                                                                                                                                                                    Sequence 11, Application US/08129456A

Patent No. 5641867

GENERAL INFORMATION:
APPLICANT: Clauss, Matchias
APPLICANT: Rao, Janet
APPLICANT: Rao, Janet
APPLICANT: Elbutti, Steven K.
ITILE OF INVENTION: Endothelial-Monocyte Activating
ITILE OF INVENTION: Polypeptide II: A Mediator Which
ITILE OF INVENTION: Activates Host Response
ITILE OF SEQUENCES: 37

CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0 Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/129,456A
FILING DATE: 29-5EP-1993
CLASSIFTCATION: 530
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 53.1%; Score 835; DB 1; Best Local Similarity 94.0%; Pred. No. 3.9e-69; Matches 156; Conservative 6; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: White, John P.
REGISTRATION NUMBER: 28,678
REGISTRATION NUMBER: 4173
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 278 0400
TELEPAX: 212 391 0526
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 166 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New York
: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: New York STATE: New York
                                                                                                                                                                                                       310 GIK 312
                                                                                                                                                                                                                                                    GIK 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: lir
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-129-456A-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                              250
                                                                                                                                                                                                                                                    181
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                                                                        120 EKKAKEKIEKKGEKKEKKQQSIAGSADSKPIDVSRLDLRIGCIITARKHPDADSLYVEEV 179
                                                                                                                                                               180 DVGEIAPRTVVSGLVNHVPLEQMQNRMVILLCNLKPAKMRGVLSQAMVMCASSPEKIEIL 239
                                                                                                                                                                                                                                                                                                                        240 APPNGSVPGDRITFDAFPGEPDKELNPKKKIWEQIQPDLHTNDECVATYKGVPFEVKGKG 299
                                                                                                                                                                                                                                                                                                                                                      238 APPNGSVPGDRITFDAFPGEPDKELNPKKKIWEQIQPDLHTNAECVATYKGAPFEVKGKG 297
                                            61 ELKOELIQAEIQNGVKQIAFPSGTPLHANSMVSENVIQSTAV-TTVSSGTKEQIKGGTGD 119
1 MATNDAVLKRLEGKGAEADQIIEYLKQQVALLKEKAILQATWREEKKLRVENAKLKKEIE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KGEKKEKKQOSIAGSADSKPIDVSRLDLRIGCIITARKHPDADSLYVEEVDVGEIAPRTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59.2%; Score 931; DB 3; Length 183; 98.4%; Pred. No. 6.4e-78; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 7, Application US/08483534A

Patent No. 6013483

GENERAL INFORMATION

APPLICANT: Coleman, Timothy A

APPLICANT: Rosen, Craig

TITLE OF INVENTION: Endothelial-Monocyte Activating

TITLE OF INVENTION: Polypeptide III

NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS: 7

COURTE OF SECURIAL STEWART & OLSTEIN

STREET: 6 BECKER FARM ROAD

STREET: 6 BECKER FARM ROAD

STREET: COUNTRY: USA

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 325800-464 (PF206)
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COMPUTER: 18M PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,534A
FILING DATE: 07 JUN 95
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAMME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKST NUMBER: 32:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 183 AMINO ACIDS TYPE: AMINO ACID
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 98.4
Matches 180; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: PROTEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 VVILCNIKPARARGVISQAMVMCASSPDKVBILAPPNGSVPGDRITFDAFPGEPDKELNP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 SKPIDASRLDIRIGCIVTAKKHPDADSLYVEEVDVGEAAPRTVVSGLVNHVPLEQMQNRM 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               147 SKPIDVSRLDLRIGCIITARKHPDADSLYVEEVDVGEIAPRTVVSGLVNHVPLEQMQNRM
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Pred. No. 3.9e-69;
6; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              267 KKKIWEQIQPDLHTNDECVATYKGVPFEVKGKGVCRAQTMSNSGIK 312
                                                                                                                                                                                                                                                                          COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.30, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/851,026
FILING DATE: 07 Amay-2001
CLASSIFICATION: vUMRIOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Famodu, Layo O.
APPLICANT: Famodu, Layo O.
TITLE OF INVENTION: Methionine Metabolic Enzymes
FILE REFERENCE: BB-1241
CURRENT APPLICATION NUMBER: US/09/392,772
CURRENT FILING DATE: 1999-09-07
EARLIER APPLICATION NUMBER: 60/099,519
EARLIER FILING DATE: 1998-09-08
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Microsoft Office 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: White, John P. REGISTRATION NUMBER: 28,678 REFERENCE/DOCKET NUMBER: 41735-A-PCT-US
                                                                                                               ADDRESSEE: Cooper & Dunham, LLP
STREET: 1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/360,821
FILING DATE: 08-OCT-96
ATTORNEY/AGENT INFORMATION:
                Libutti, Steven K
TITLE OF INVENTION: Endothelial Monoc
Polypeptide II:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 10, Application US/09392772; Patent No. 6346403; GENERAL INFORMATION:
                                                                                                                                                                                                               ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 212-278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53.1%;
94.0%;
                                                                             NUMBER OF SEQUENCES: 42
                                                                                              CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 94.0°
Matches 156; Conservative
                                                                                                                                                    CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-392-772-10
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                                                                               Sequence 11. Application US/08360821B
Sequence 11. Application US/08360821B
Set of 222837
GENERAL INFORMATION:
APPLICANT: Stern, David M.
APPLICANT: Kay Matchias
APPLICANT: Kay on, Mark
APPLICANT: Kay on, Mark
APPLICANT: Libuti, Steven K
APPLICANT: Libuti, Libuti, LLP
STREET: 1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             147 SKPIDVSRLDLRIGCIITARKHPDADSLYVEEVDVGEIAPRTVVSGLVNHVPLEQMQNRM 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               207 VILLCNLKPAKMRGVLSQAMVMCASSPEKIEILAPPNGSVPGDRITFDAFPGEPDKELNP 266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 166;
121 KKKIWEQIQPDLHTNAECVATYKGAPFEVKGKGVCRAQTMANSGIK 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                              53.1%; Score 835; DB 3;
94.0%; Pred. No. 3.9e-69;
tive 6; Mismatches 4;
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Patent No. 6734168
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Stern, David M. Clauss, Matthias
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 212-591-00-1 INFORMATION FOR SEQ ID NO: 11: SEQUENCE CHARACTERISTICS: LENGTH: 166 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 94.0
Matches 156; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: Peptide
                                                                                                                                                                                                                                                                                                                                                                                   CITY: New York
STATE: New York
COUNTRY: USA
                                                            RESULT 12
US-08-360-821B-11
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US-09-851-026-11
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Gaps 11;
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                                                                                                                                                                                                                                                                                                                                                                                                 |----TKLSDGGTKKEPKKQS--GGSKSKTABADITVAKLDIRVGLIRKAEKHPDADSLY 521
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                                                                                                                                                                                                                                                                                                                                 430 LKDE-----DVALHREKYAGSQAERSSKAAADAEANKVANQLKG---- 468
                                                                                                                                                                                                                                                                                                                                                                            120 EKKAKEKIEKKGEKKEKKQQSIAGSADSK----PIDVSRLDLRIGCIITARKHPDADSLY 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                            VEEVDVGETAPRIVVSGLVNHVPLEQMQNRMVILLCNLKPAKMRGVLSQAMVMCASSPE- 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   235 -KIEILAPPNGSVPGDRITFDAFPGEPDKELNPKKKIWEQIQPDLHTNDECVATYKGVPF 293
                                                                                                                                                                 63;
                                                                                                                          DB 3; Length 659;
                                                                                                                        Query Match 32.5%; Score 510.5; DB 3; Length 6 Best Local Similarity 38.6%; Pred. No. 2.3e-38; Matches 123; Conservative 49; Mismatches 84; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Coleman, Roger
APPLICANT: Au-Young, Janice
APPLICANT: Murry, Lynn E.
TITLE OF INVENTION: NOVEL MONOCYTE ACTIVATING CYTOKINE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                          18 ADQIIEYLKQQVSLLKEKAILQATLREEKKLRVENAKLKKE---
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ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPUTED:
CORPATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/705,868
FILING DATE: Filed Herewith
ATTORNEY/ABRIT INFORMATION:
MAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: PF-0117 US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               294 EVKGKGVCRAQTMSNSGIK 312
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 301 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       415-845-4166
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CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
                                      TYPE: PRT
ORGANISM: Zea mays
US-09-392-772-10
                     LENGTH: 659
SEQ ID NO 10
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123 AKEKIEKKGEKKEKKQQSIA-GSA-DSKPIDV--SRLDLRIGCIITARKHPDADSLYVEE 178
                                                                                                                                                                           179 VDVGEIAPRIVVSGLVNHVPLEQMQNRMVILLCNLKPAKMRGVLSQAMVMCASSP---EK 235
                                                                                                                                                                                                                                                                               236 IEILAPPNGSVPGDRITFDAF-PGEPDKELNPKKKIWEQIQPDLHINDECVATYKGVPFE 294
                                                                                                                                                                                                                                                                                             9
                                                                                                  Length 301;
                                                                                                                                Indels
                                                                                                ch 28.0%; Score 440.5; DB 2; 1 Similarity 49.5%; Pred. No. 2e-32; 94; Conservative 36; Mismatches 51;
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            MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY:
CLONE: Consensus
                                                                                                                                                                                                                                                                                                                                         295 VK-GKGVCRA 303
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TOPOLOGY: linear
                                                                                                  Query Match
Best Local Similarity
Matches 94; Conserv
                                                                      US-08-705-868-1
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Sequence 2, Appli Sequence 183003, Sequence 37579, A Sequence 350231, Sequence 2, Appli Sequence 2, Appli

22.09 23.22.09 23.22.09 23.22.09 23.22.09 24.40 24.40 25.40 25.40 26.40 27.40

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Sequence 2, Appli Sequence 372, App Sequence 132, App

6 US-10-425-115-350232 6 US-10-437-963-183001 0 US-09-930-169-2 6 US-10-423-730-2 6 US-10-425-114-37579 6 US-10-425-115-350231 0 US-09-813-718-2 6 US-10-240-527A-2 6 US-10-240-532-2 6 US-10-240-532-2 6 US-10-240-532-6 6 US-10-318-6 7 US-09-813-718-6 8 US-10-310-44089 105-09-813-718-6 105-09-813-718-6 105-09-813-718-6 105-09-813-718-6 105-10-410-425-115-3595 105-10-425-115-327897 105-10-425-115-327897 105-10-425-115-327897 105-10-425-115-327897 105-10-425-115-327897 105-10-425-115-327897 105-10-425-115-327897 105-10-425-115-327897 105-10-425-115-327897 105-10-425-115-327897 105-10-425-115-327897 105-10-425-115-327897 105-10-425-115-327897 105-10-425-115-327897

223.00 233.00 233.00 233.00 233.00 233.00

Sequence 6, Appli Sequence 6, Appli Sequence 2, Appli Sequence 157861, Sequence 197042, Sequence 197042, Sequence 35195, A Sequence 31191, Sequence 36181, Sequence 36188, Sequence 240858, Sequence 240858, Sequence 240858, Sequence 240858, Sequence 2585, A

Sequence 22, Appl Sequence 22, Appl Sequence 22, Appl Sequence 30, Appl

US-10-240-532-22 US-10-240-527A-22 US-10-425-115-304067 US-10-425-115-197045 US-10-424-599-157865

221.5 220.1 18.6 18.6 18.6 16.1

Sequence 197045, Sequence 157860,

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Sequence 11, Appl
Sequence 11, Appl
Sequence 3, Appli
Sequence 3, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 180396,
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Sequence 36, Appl
Sequence 35, Appl
Sequence 7, Appli
Sequence 11, Appli
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                                                                                                                                    (without alignments)
764.514 Million cell updates/sec
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                                                                                                                                                                                  US-10-623-567A-1
1573
1 MANNDAVLKRLEQKGAEADQ.....FEVKGKGVCRAQTWSNSGIK
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                                                                                                                 August 3, 2005, 21:51:44 ; Search time 159 Seconds
               GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-09-851-026-36

US-09-851-026-36

US-09-851-026-37

US-09-851-026-37

US-09-9851-026-11

US-09-930-169-3

6 US-10-823-730-3

6 US-10-823-730-1

6 US-10-823-730-1

6 US-10-823-730-1

6 US-10-424-599-180396
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Maximum Match 100%
Listing first 45 summaries
                                                                                   OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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1568
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1343
951
835
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709
709
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                                                                                                                                                                                                                       Sequence:
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    US-10-494-940-4/
Sequence 47, Application US/1049490
FULLICATION. US2005006986A1
GENERAL INFORMATION:
APPLICANT: OriGene Technologies, Inc
TITLE OF INVENTION: REGULATED PROSTATE CANCER GENES
FILE REFERENCE: OGT 9U 803 PCT
CURRENT APPLICATION NUMBER: US/10/494,940
CURRENT FILING DATE: 2004-05-07
FRIOR APPLICATION NUMBER: 60/331,041
FRIOR APPLICATION NUMBER: 60/331,041
FRIOR FILING DATE: 2001-11-07
FRIOR FILING DATE: 2001-11-07
FRIOR FILING DATE: 2001-12-18
FRIOR APPLICATION NUMBER: 60/340,251
FRIOR APPLICATION NUMBER: 60/344,791
FRIOR FILING DATE: 2002-01-07
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Best Local Similarity 100.
Matches 312; Conservative
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US-10-494-940-47
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Result ģ

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Patent No. US20020160957A1
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                                                                                     KKAKEKIEKKGEKKEKKQOSIAGSADSKPIDVSRLDLRIGCIITARKHPDADSLYVEEVD 180
                                                                                                                                                      VGEIAPRIVVSGLVNHVPLEQMQNRMVILLCNLKPAKMRGVLSQAMVMCASSPEKIEILA 240
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                      ELKQELIQAEIQNGVKQIAPPSGTPLHANSMVSENVIQSTAVTTVSSGTKEQIKGGTGDE 120
                                                                                                                                   VGEIAPRIVVSGLVNHVPLEQMQNRMVILLCNLKPAKMRGVLSQAMVMCASSPEKIEILA 240
                                                                                                                                                                                                      PPNGSVPGDRITFDAFPGEPDKELNPKKKIWEQIQPDLHTNDECVATYKGVPFEVKGKGV 300
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                                                                    KKAKEKI EKKGEKKEKKQQS I AGSADSKPI DVSRLDLR I GCI I TARKHPDADSLYVEEVD
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Sequence 1, Application US/10623567A

Publication No. US20050119175A1

GENERAL INFORMATION:

APPLICANT: Kim, Sunghoon

TITLE OF INVENTION: Method for Stimulating Wound Healing
FILE REFERENCE: 012679-093

CURRENT APPLICATION NUMBER: US/10/623,567A

CURRENT FILING DATE: 2003-07-22

PRIOR PILING DATE: 2002-07-22

NUMBER OF SEQ ID NOS: 7

SOFTWARE: PastSEQ for Windows Version 4.0

SEQ ID NO 1

LENGTH: 312
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100.0%; Pred. No. 1.2e-118;
tive 0; Mismatches 0;
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Matches 312; Conservative
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CORGANISM: Homo sapiens
US-10-623-567A-1
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US-09-851-026-36 ; Sequence 36, Application US/09851026

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Kao, curre
Kayton, Mark
Libutti, Steven K
TITLE OF INVENTION: Bndothelial Monocyte Activating
Polypeptide II: A Mediator Which Activates Host Response
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 BLKQELIQAEIQNGVKQIAFPSGTPLHANSMVSENVIQSTAVTTVSSGTKEQIKGGTGDE 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 VGEIAPRTVVSGLVNHVPLEQMQNRMVILLCNLKPAKMRGVLSQAMVMCASSPEKIEILA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MANNDAVLKRLEQKGAEADQIIEYLKQQVSLLKEKAILQATLREEKKLRVENAKLKKEIE
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                                                                                                                                                                                                                                                                                                                                       ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.30, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/360,821
FILIND DATE: 08-OCT-96
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 241735-A-PCT-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
99.7%; Score 1568; DB 9;
Best Local Similarity 99.7%; Pred. No. 3e-118;
Matches 311; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                    STREET: 1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
REPLICATION NUMBER: US/09/851,026
FILING DATE: 07-May-2001
CLASSIFICATION: «UMKNOWN»
                                                                                                                                                                                                                          ADDRESSEE: Cooper & Dunham, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 36:
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TELEPHONE: 212-278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 312 amino acids
                APPLICANT: Stern, David M. Clauss, Matthias Kao, Janet
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STATE: New York
                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
GENERAL INFORMATION:
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Sequence 11, Application US/09851026
Patent No. US20020160957A1
GENERAL INFORMATION:
APPLICANT: Stern, David M.
Kao, Janet
Kao, Janet
Kao, Janet
Libutti, Steven K
TITLE OF INVENTION: Endothelial Monocyte Activating
Polypeptide II: A Mediator Which Activates Host
238 APPNGSVPGDRITFDAFPGEPDKELNPKKKIWEQIQPDLHTNAECVATYKGAPFEVKGKG 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
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; Sequence 7, Application US/20050048616A1
; Publication No. US20050048616A1
; GENERAL INFORMATION:
    APPLICANT: Coleman et al.
; TITLE OF INVENTION: Endothelial Monocyte Activating Polypeptide III
; FILE REFERENCE: PF206D1
; CURRENT APPLICATION NUMBER: US/10/910,403
; CURRENT FILING DATE: 2004-08-04
; PRIOR APPLICATION NUMBER: US/08/972,301
; PRIOR APPLICATION NUMBER: US/08/483,534
; PRIOR APPLICATION NUMBER: US/08/483,534
; NUMBER OF SEQ ID NOS: 195-06-07
; SOFTWARE: Patentin version 3.0
; SSQ ID NOS: 7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 951; DB 17;
Pred. No. 9.9e-69;
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham, LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
60.5%; Score 951; DB
Best Local Similarity 100.0%; Pred. No. 9.9
Matches 183; Conservative 0; Mismatches
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                            298 VCRAQTMANSGIK 310
                                                    300 VCRAQTMSNSGIK 312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   310 GIK 312
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US-09-851-026-11
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                                                                                                 Sequence 35, Application US/09851026
Patent No. US20020160957A1
GENERAL INFORMATION:
APPLICANT: Stern David M. .
Kayton, Matchias
Kao, Janet
Kayton, Matchias
Libutti, Steven K
TITLE OF INVENTION: Endothelial Monocyte Activating
Polypeptide II: A Mediator Which Activates Host Response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DVGEIAPRTVVSGLVNHVPLEQMQNRMVILLCNLKPAKMRGVLSQAMVMCASSPEKIEIL 239
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85.9%; Pred. No. 4.5e-100;
tive 13; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.30, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/851,026
FILING DATE: 07-May-2001
CLASSIFICATION NUMBER: US/08/360,821
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/360,821
FILING DATE: 08-0CT-96
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41735-A-PCT-US
TELEPHONE: 212-231-0525
INFORMATION FOR SEQ ID NO: 35:
                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham, LLP
STREET: 1185 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: single
STRANDEDNESS: single
STRANDEDNESS: single
STRANDEDNESS: single
SEQUENCE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 35:
US-09-851-026-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 310 amino acids
                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 85.9%
Matches 269; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
                                                                                 .09-851-026-35
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US-09-930-169-1

Sequence 1, Application US/09930169

Sequence 1, Application No. US20030004309A1

Sequence 1, Application No. US20030004309A1

GENERAL INFORMATION:

APPLICANT: KIM, SUNGHOON

APPLICANT: KIM, SUNGHOON

TITLE OF INVENTION: HAWINOLOGICAL ENHANCEMENT AGENT COMPRISING N-TERMINAL PEPTIDE OF TITLE OF INVENTION: P43 AS AN EFFECTIVE COMPONENT

TITLE OF INVENTION: P43 AS AN EFFECTIVE COMPONENT

TITLE OF INVENTION: P43 AS AN UMBER: US/09/930,169

CURRENT APPLICATION UNMBER: KR 2001-08-16

PRIOR FILING DATE: 2001-08-16

PRIOR FILING DATE: 2001-06-05

NUMBER OF SEQ ID NOS: 11

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/10823730
; Sequence 3, Application US/10823730
; Publication No. US20040185060A1
; GENERAL INFORMATION:
    APPLICANT: IMAGENE CO., LTD.
    TITLE OF INVENTION: Immunological enhancement agent comprising N-terminal peptide of TITLE OF INVENTION: p43 as an effective component
    TITLE OF INVENTION: D43 as an effective component
    TITLE OF INVENTION: D43 as an effective component
    CURRENT APPLICATION NUMBER: US/10/823,730
    CURRENT PILING DATE: 2004-04-14
    NUMBER OF SEQ ID NOS: 11
    SOFTWARE: Kopatentin 1.71
    SEQ ID NO 3
    LENGTH: 166
                                                                                                                      61 DVSRLDLRIGCIITARKHPDADSLYVEEVDVGEIAPRTVVSGLVNHVPLEQMQNRMVILL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           151 DVSRLDLRIGCIITARKHPDADSLYVEEVDVGEIAPRTVVSGLVNHVPLEQMQNRMVILL 210
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91 MVSENVIQSTAVTTVSSGTKEQIKGGTGDEKKAKEKIEKKGEKKEKKQQSIAGSADSKPI
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                                                                                                                                                                                             CNLKPAKMRGVLSQAMVMCASSPEKIEILAPPNGSVPGDRITFDAF 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      211 CNLKPAKMRGVLSQAMVMCASSPEKIEILAPPNGSVPGDRITFDAF 256
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52.8%; Score 831; DB 16;
Best Local Similarity 100.0%; Pred. No. 4.3e-59;
Matches 166; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Unknown Organism
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US-10-823-730-3
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Publication No. US20030004309A1
| Publication No. US20030004309A1
| GENERAL INFORMATION:
| APPLICANT: KIM, SUNGHOON
| APPLICANT: KIM, SUNGHOON
| TITLE OF INVENTION: P43 AS AN EFFECTIVE COMPONENT
| TITLE OF INVENTION: P43 AS AN EFFECTIVE COMPONENT
| FILE REFERENCE: 058333/0106
| FILE REFERENCE: 058333/0106
| FILE REFERENCE: 2001-08-16
| PRIOR APPLICATION NUMBER: KR 2001-31310
| PRIOR APPLICATION NUMBER: KR 2001-31310
| NUMBER OF SEQ ID NOS: 11
| SOFTWARE: Patentin Ver. 2.1
| SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    147 SKPIDVSRLDLRIGCIITARKHPDADSLYVEEVDVGEIAPRTVVSGLVNHVPLEQMQNRM 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 VVLLCNLKPAKWRGVLSQAWVMCASSPDKVEILAPPNGSVPGDRITFDAFPGEPDKELNP 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       267 KKKIWEQIQPDLHTNDECVATYKGVPFEVKGKGVCRAQTMSNSGIK 312
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                                       Version #1.30
                                                        CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/851,026
FILING DATE: 07-May-2001
CLASSIFICATION DATA:

APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/360,821
FILING DATE: 08-0CT-96
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41735-A-PCT-US
TELEPHONE: 212-278-0400
TELEPHONE: 212-378-0400
TELEPHONE: 212-391-0525
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
TENDOTH: 166 amino acids
TYNES: AMINO acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 52.8%; Score 831; DB 10;
Best Local Similarity 100.0%; Pred. No. 4.3e-59;
Matches 166; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53.1%; Score 835; DB 9; 94.0%; Pred. No. 2e-59; tive 6; Mismatches 4.
           OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.30,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
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ORGANISM: Unknown Organism
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Best Local Similarity 94.0
Matches 156; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-851-026-11
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US-09-930-169-3
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91 MVSENVIQSTAVTTVSSGTKEQIKGGTGDEKKAKEKIEKKGEKKEKKQQSIAGSADSKPI 150

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Sequence 350232, Application US/10425115

Publication No. US20040214272A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

APPLICANT: Cao, Yon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 LKQELIQAEIQNGVKQIAPPSGTPLHANSMVSENVIQSTAVTTVSSGTK--EQIKGGTGD 119
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                                                                                                                                                                                                                             148 LKDE-----DVALHREKYAGSQAERSSKAAADAEANKVANQLKG----
                                                                                                                                                                                           56 KKEIEELKOELIQAEIQNGVKQIAFPSGTPLHANSMVSENVIQSTAVTTVSSGTKEQIKG
                                                                                                                                                                                                                                                                                                                                                                                                                176 VEEVDVGEIAPRIVVSGLVNHVPLEQMQNRMVILLCNLKPAKMRGVLSQAMVMCASSPE-
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                                                                                   Length 353;
                                                                                                                                         Indels
; OTHER INFORMATION: Clone ID: PAT_MRT3847_133912C.1.pep
US-10-424-599-180396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18 ADQIIEYLKQQVSLLKEKAILQATLREEKKLRVENAKLKKE-
                                                                                   Query Match 33.6%; Score 528; DB 15; Best Local Similarity 43.6%; Pred. No. 3.5e-34; Matches 113; Conservative 41; Mismatches 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Clone ID: MRT4577_82583C.1.pep
US-10-425-115-350232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (1)..(377)
OTHER INFORMATION: unsure at all Xaa locations
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ORGANISM: Zea mays
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Publication No. US20040185060A1
GENERAL INFORMATION:
APPLICANT: IMAGENE CO., LTD.
TITLE OF INVENTION: DA3 as an effective component
FILE REFERENCE: NPPIJ18
CURRENT APPLICATION NUMBER: US/10/823,730
CURRENT FILING DATE: 2004-04-14
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Kopatentin 1.71
SUCIDENT APPLICATION NUMBER: US/10/823,730
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Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: APPLICANT: ADOUT WITHOUS APPLICANT:
APPLICANT: Cato Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 180396
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                                                                                                                     1 MANNDAVLKRLEQKGAEADQIIEYLKQQVSLLKEKAILQATLREEKKLRVENAKLKKEIE
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        45.1%; Score 709; DB 10; Length 147; 100.0%; Pred. No. 2.6e-49; ive 0; Mismatches 0; Indels (
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Matches 147; Conservative
                                       Best Local Similarity 100.
Matches 147; Conservative
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ORGANISM: Glycine max
PEATURE:
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ORGANISM: mammalian
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US-10-424-599-180396
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US-10-823-730-1
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TYPE: PRT
ORGANISM: Unknown Organism
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US-10-823-730-2
                                                                                                                                                                                  SEQ ID NO 2
LENGTH: 108
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US-10-823-730-2
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Sequence 183001, Application US/10437963

Sequence 183001, Application US/10437963

Sequence 183001, Application US/10437963

Sequence 183001, Application US/104373434

APPLICANT: La Rosa, Thomas J.

APPLICANT: Cao, Yongwei

APPLICANT: Boukharov, Andrey A.

APPLICANT: Bukharov, Andrey A.

APPLICANT: Bring Harbaruk, Bard

APPLICANT: Li, Ping

TITLE OF INVENTION: Plant and Uses Thereof for Plant Improvement

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REPERENCE: 38-21(53221)B

CURRENT APPLICATION NUMBER: US/10/437,963

CURRENT APPLICATION NUMBER: US/10/437,963

SEQ ID NO 183001

LENGTH: 804
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527 EVLLQLNMTPEESLSFCDDKGEIAKARRPWDFVSAGHKIGKPSPLFKELKDEEVES---- 582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  188 TVVSGLVNHVPLEQMQNRMVILLCNLKPAKMRGVLSQAMVMCASSPE--KIEILAPPNGS 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            246 VPGDRITFDAFPGEPDKELNPKKKIWEQIQPDLHTNDECVATYKGVPFEVKGKGVCRAQT 305
                                  235 -KIEILAPPNGSVPGDRITFDAFPGEPDKELNPKKKIWEQIQPDLHTNDECVATYKGVPF 293
                                                          74 GVKQIAFPSGTPLHANSMVSENVIQSTAVTTVSSGTK--EQIKGGTGDEKKAKEKIEKKG 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        132 EKKEKKQQSIAGSADSK----PIDVSRLDLRIGCIITARKHPDADSLYVEEVDVGEIAPR 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               240 VEEIDVGEDTPRTVVSGLVKFIPLEEMQNRKVCVLCNLKPVAMRGIKSHAMVLAASNEDH 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35 KAILQATLREEKKL----RVENAKLKKE-------IEELKQELIQAEIQN 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 804;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Clone ID: PAT_MRT4530_80132C.1.pep
US-10-437-963-183001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 38.1%; Pred. No. 8.4e-33;
Matches 117; Conservative 53; Mismatches 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 2, Application US/09930169; Publication No. US20030004303A1 GENERAL INFORMATION: APPLICANT: KIM, SUNGHOON
                                                                                                            294 EVKGKGVCRAQTMSNSGIK 312
                                                                                                                                    360 TTSA-GICKVKTIANGEIR 377
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IASGEIR 804
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US-09-930-169-2
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Sequence 2, Application US/10823730
Publication No. US20040185060A1
GENERAL INFORMATION:
APPLICANT: IMAGENE CO., LTD.
TITLE OF INVENTION: p43 as an effective component
TITLE OF INVENTION: D43 as an effective component
TITLE OF INVENTION: D43 as an effective component
CURRENT APPLICATION NUMBER: US/10/823,730
CURRENT FILING DATE: 2004-04-14
NUMBER OF SEQ ID NOS: 11
SEQ ID NO 2
LENGTH: 108
TITLE OF INVENTION: P43 AS AN EFFECTIVE COMPONENT
TITLE OF INVENTION: P43 AS AN EFFECTIVE COMPONENT
TITLE OF INVENTION: P43 AS AN EFFECTIVE COMPONENT
FILE REFERENCE: 088333/0106
CURRENT APPLICATION NUMBER: US/09/930,169
CURRENT FILING DATE: 2001-08-16
PRIOR APPLICATION NUMBER: KR 2001-31310
PRIOR FILING DATE: 2001-06-05
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PATENTIN Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                            PEATURE:
OTHER INFORMATION: Description of Unknown Organism: Mammalian
OTHER INFORMATION: protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 32.8%; Score 516; DB 16; Length 108; Best Local Similarity 100.0%; Pred. No. 6.5e-34; Matches 108; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 32.8%; Score 516; DB 10; Length 108; Best Local Similarity 100.0%; Pred. No. 6.5e-34; Matches 108; Conservative 0; Mismatches 0; Indels
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Job time : 161 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

August 3, 2005, 21:45:34 ; Search time 174 Seconds Run on:

(without alignments)
918.211 Million cell updates/sec

US-10-623-567A-1 1573 Perfect score:

1 MANNDAVLKRLEQKGAEADQ.......FEVKGKGVCRAQTMSNSGIK 312 Sequence:

Gapop 10.0 , Gapext 0.5 BLOSUM62 Scoring table:

1612378 segs, 512079187 residues Searched:

1612378 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt\_03:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Q12904 homo sapien		P31230 mus musculu	mus musc			Q7q8s7 anopheles g		-				Q6dfz7 brachydanio	ın		-		schizosa	Q7zx51 xenopus lae	Q6dij1 xenopus tro		_		Q6cki6 kluyveromyc					droso	8 oryza s	Q9epv3 rattus norv
SUMMARIES		MCA1 HUMAN	MCA1 CRIGR	MCA1 MOUSE	Q8C2 <u>U</u> 7	Q7ZWY7	Q9V504	Q7Q8S7	SYM CABEL	SYM_ORYSA	062542	SYM ARATH	QeTGS6	Q6DF27	SYYC BOVIN	SYYC_HUMAN	SYYC_MOUSE	Q6BY38	Q9P6K7	Q72X51	Q6DIJ1	G4P1_YEAST	Q6FNN0	Q754V3	Q6CKI6	QBRUPB	Q6C763	Q93VB0	Q7XJM9	090060	Q7XVQ8	Q9EPV3
	DB	<u>:</u> -	Н	Н	7	N	7	~	-	-	7	-	~	7	1	Н	Н	~	7	~	~	~	~	~	~	N	~	7	~	7	~	7
	Length	312	359	310	319	297	323	351	917	804	149	797	529	529	527	527	527	373	450	528	528	376	376	371	372	409	394	389	440	525	252	78
d	Query Match	100.0	9.98	85.4	85.1	68.9	42.7	39.8	35.9	32.9	31.8	31.7	28.8	28.7	28.6	28.6	28.4	28.1	28.1	28.0	27.9	27.3	27.1	26.9	26.4	25.6	25.5	25.5	25.5	25.1	24.9	24.7
	Score	1573	1362.5	1343	1338	1084	671	625.5	564	517	499.5	499	453.5	451.5	450	450	446.5	441.5	441.5	440	439	429	426	423.5	415	402	401.5	400.5	400.5	395	391	388
	Result No.	1	7	٣	4	5	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31

Q78ac3 neurospora Q9m1x8 arabidopsis O97487 euplotes oc Q7qd89 anopheles g Q8i148 plasmodium Q7rka7 plasmodium Q7rka7 plasmodium Q7r21 pyrococcus Q6btq8 debaryomyce Q9v011 pyrococcus O58721 pyrococcus O58721 pyrococcus O58721 pyrococcus O58721 pyrococcus Q72ac2 desulfovibr Q6fe35 acinetobact Q72at8 treponema d Q72148 thermus the
075AC3 09M1X8 097487 070B89 08IL48 0RKA7 SYM PYRFU 06BTQ8 SYM PYRAB SYM PYRAB O72AE2 072AE2
44444444444444444444444444444444444444
4413 44413 4402 4402 4403 722 722 723 665 618
224.11.12.22.23.33.33.33.33.33.33.33.33.33.33.33
378.5 337.5 318.5 292.5 201.5 227 227 223.5 212 209.5 207.5
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## ALIGNMENTS

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MEDINE-2538825; PubMed=12477932; DOI=10.1073/pnas.242603899; MEDINE-2538825; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D., Alackul S.F., Zeberge B. Buetcow K.H., Schaefer C.F., Bhar N.K., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Biatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Saares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshivuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Raha S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Narchards S., Worley K.C., Hale S., Garcia A., Gibbs R.A., Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G., Mhiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butkefley R.W., Krzywinski M.I., Skalska U., Smailus D.E., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Marra M.A., Schein J.B., Jones S.J.M., Marra M.A., Schein J.B., Jones J.M., Marra M.A., Schein J.B., Jones S.J.M., Marra M.A., Schein J.B., Jones J.M., Marra M.A., Schein J.M., J.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=95014290; PubMed=7929199;
MEDLINE=95014290; PubMed=7929199;
Kao J., Hauck K., Fan Y., Haehnel I., Libutti S.K., Kayton M.L.,
Grikscheit T., Chabot J., Nowygrod R., Greenberg S., Kuang W.J.,
Leung D.W., Hayward J.R., Kisiel W., Heath M., Brett J., Stern D.M.;
"Characterization of a novel tumor-derived cytokine. Endothelial-
monocyte activating polypeptide II.";
J. Biol. Chem. 269:25106-25119(1994).
                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                          012904; 096C09;
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 45, Last sequence update)
25-0CT-2004 (Rel. 45, Last annotation update)
Multisynthetase complex auxiliary component p43 [Contains:
Endothelial-monocyte activating polypeptide II (EMAP-II) (Small
inducible cytokine subfamily E member 1)].
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312 AA.
   PRT;
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   STANDARD;
                                                                                                                                                                                                                                                                                                     Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
   MCA1 HUMAN
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1 MANNDAVLKRLEQKGAEADQIIEYLKQQVSLLKEKAILQATLREEKKLRVENAKLKKEIE
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      and for commercial
                 (See http://www.isb-sib.ch/announce/
                                                                                                                                                                               GO; GO:0005615; C:extracellular space; TAS.
GO; GO:0005615; F:cytokine activity; TAS.
GO; GO:000649; F:rENAA binding; TAS.
GO; GO:000695; P:chemctaxis; TAS.
GO; GO:0006954; P:inflammatory response; TAS.
GO; GO:0006918; P:rENAA aminoacylation for protein translation; TAS.
InterPro; IPR008232; EMAPII.
InterPro; IPR002894; Nucleic acid OB.
InterPro; IPR002894; Nucleic acid OB.
Fram, PF01589; FRAA bind.
Fram, PF01589; TRAA bind.
PENSF; PIRSF005381; EMAPII; 1.
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polypeptide II.
FRNA-binding.
A -> P (in Ref. 2).
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tRNA-binding.
PROPEP 1 146
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      Usage by
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    modified and this statement is not removed.
                    entities requires a license agreement ( or send an email to license@isb-sib.ch)
                                                         EMBL; U10117; AAA62202.1; -- EMBL; BC014651; AAH14051.1; -- PDB; 1E7Z; X-ray; A=147-312. PDB; 1EUU; X-ray; A/B=147-312. PDB; 1EUU; X-ray; A/B=147-312. PDB; 1FLO; X-ray; A=150-312. PDB; 1FLO; X-ray; A=150-312. PLIN'DB; HX0004426; -- PLIN'DB; HX0004426; -- PLIN'DB; 
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312 AA;
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Best Local Similarity
Matches 312; Conserv
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                                                                                               KKAKEKIEKKGEKKEKKQQSIAGSADSKPIDVSRLDLRIGCIITARKHPDADSLYVEEVD 180
                                                                                                                                                                                                                               PPNGSVPGDRITFDAFPGEPDKELNPKKKIWEQIQPDLHTNDECVATYKGVPFEVKGKGV 300
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                                                                                                                                                                                                                                                 II Cytokine.";
J. Biol. Chem. 272:32573-32579 (1997).
J. Biol. Chem. 272:32573-32579 (1997).
J. Biol. Chem. 272:32573-32579 (1997).
J. Biol. Component of the multisynthetase complex which is comprised of a bifunctional glutamyl-prolyl-tRNA synthetase, the monospecific isoleucyl, leucyl, glutaminyl, methionyl, lysyl, arginyl, and aspartyl-tRNA synthetases as well as three auxiliary proteins, pl8, p48 and p43.

J. SIMILARITY: Contains 1 tRNA-binding domain.
                                                                                                                                                                             VŒI APRIVVSGLVNHVPLEQMQNRMVILLCNLKPAKMRGVLSQAMVMCASSPEKIEILA
ELKQELIQAEIQNGVKQIAFPSGTPLHANSMVSENVIQSTAVTTVSSGTKEQIKGGTGDE
                                                                                                                                                       VGEIAPRTVVSGLVNHVPLEQMQNRMVILLCNLKPAKMRGVLSQAMVMCASSPEKIEILA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Multisynthetase complex auxiliary component p43 [Contains:
Endothelial-monocyte activating polypeptide II (EMAP-II) (Small inducible cytokine subfamily E member 1)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE=98070438; PubMed=9405472; DOI=10.1074/jbc.272.51.32573; Quevillon S., Agou F., Robinson J.-C., Mirande M.; "The p43 component of the mammalian multi-synthetase complex is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF021800; AAB95207.1; -.
HSSP; Q12904; 1B72.
InterPro; IPR008232; EMAPI.
InterPro; IPR008232; EMAPI.
InterPro; IPR008234; Nucleic acid_OB.
InterPro; IPR0082547; tRNA_bind.
PHOST: PRSF00581; EMAPI: 1.
PROSITE; PS50886; TRBD; 1.
Cytokine; Protein blosynthesis; RNA-binding, tRNA-binding.
I 194 By similarity.
CHAIN
CHAIN
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Eukaryota, Metazoa, Chordata, Crania
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                                                                                                                                                                                                                                                                                                                                    STANDARD;
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Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A ploting R.F., Jordan H., Moorer T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Richards S., Worlby K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Yullalon D.K., Murny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
                                                                                                                                                                                                                              226 VDVGEAAPRTVISGLVNHVPLDQMQNRMVVLLCNLKPAKMRGILSQAMVMCASSPEKVEI 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LAPPNGSVPGDRITFDAFPGEPDKELNPKKKIWEQIQPDLHTNDECVATYKGVPFEVKGK 298
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Kao J., Houck K., Fan Y., Haehnel I., Libutti S.K., Kayton M.L.,
Kao J., Houck K., Fan Y., Nowygrod R., Greenberg S., Kuang W.J.,
Leung D.W., Hayward J.R., Kisiel W., Heath M., Brett J., Stern D.M.;
"Characterization of a novel tunor-derived cytokine. Endothelial-
"The activating polypeptide II.";
J. Biol. Chem. 269:25106-25119(1994).
                                                                                                                                                    Gaps
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Sciurognathi; Muridae; Murinae; Mus.
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Endothelial-monocyte activating polypeptide II (EMAP-II) (Small
inducible cytokine subfamily E member 1)].
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                                                                                              86.6%; Score 1362.5; DB 1; Length 359; 86.0%; Pred. No. 6.4e-71;
                                                                                                                                               22; Indels
                         tRNĀ-binding.
4D868D1B65D72C23 CRC64;
                                                                                                                        ; Pred. No. 6.4e-71; 19; Mismatches 22
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  polypeptide II.
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Mammalia, Eutheria, Rodentia,
                                                     39601 MW;
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                              198 . 3
359 AA;
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                                                                                                                                                                                                                                                                                         SEQUENCE OF 145-164 FROM N.A. MEDLINE=39015897; Pubmed=1400342; MEDLINE=39015897; Pubmed=1400342; Kao J., Ryan J., Brett G., Chen J., Shen H., Fan Y.-G., Godman G., Familletti P.C., Wang F., Pan Y.-C.E., Stern D., Clauss M.; Endchellal monocyte-activating polypeptide II. A novel tumor-derived polypeptide that activates host-response mechanisms."; J. Biol. Chem. 267:20239-20247(1992).
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schnerto A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=9413665; PubMed=7545917;

Kao J., Fan Y., Haehnel I., Brett J., Greenberg S., Clauss M.,

Kayton M., Houck K., Kisiel W., Seljelid R., Burnier J., Stern D.;

A peptide derived from the amino terminus of endothelial-monocyte-
activating polypeptide II modulates mononuclear and polymorphonuclear
leukocyte functions, defines an apparently novel cellular interaction
site, and induces an acute inflammatory response.";
J. Biol. Chem. 269:9774-9782(1994).

-!- FUNCTION: Alters endothelial and monocyte functions, induces the
migration of monocytes and granulocytes, and induces an
inflammatory response in the mouse footpad model. EMAP II elicits
a phlogogenic response and, potentially, augments the effects of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gape
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PIRSF005381; EMAPII; 1.
Cycoxine; PS50886; TRBD; 1.
Cycoxine; Protein biosynthesis; RNA-binding; tRNA-binding.
PROPEP
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                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1343; DB 1;
Pred. No. 7.3e-70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBUNIT: Monomer.-!- SIMILARITY: Contains 1 tRNA-binding domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polypeptide II.
tRNA-binding.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a phlogogenic response and, potent:
the other tumor-derived cytokines.
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Interpro; IPR008994; Nucleic_acid_OB.
Interpro; IPR002547; tRNA_bind.
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85.9%;
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HSSP; Q12904; 1EUJ.
MGD; MGI:102774; Scyel.
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Xenopodinae; Xenopus
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TISSUE=Embryo;
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                       DVGEIAPRTVVSGLVNHVPLEQMQNRMVILLCNLKPAKMRGVLSQAMVMCASSPEKIEIL 239
                                                                         240 APPNGSVPGDRITFDAFPGEPDKELNPKKKIWEQIQPDLHTNDECVATYKGVPFEVKGKG 299
                                                                                                 297
EKKVKEKTEKKGEKKE-KQQSAAASTDSKPIDASRLDLRIGCIVTAKKHPDADSLYVEEV 177
                                                                                                                                                                                                                                                    01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus 2 days neonate thymus thymic cells cDNA, RIKEN full-
length enriched library, clone:B43001B22 product:endothelial monocyte
activating polypeptide 2, full insert sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630 (2000).
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                                                                                        STRAIN=NOD; TISSUE=Thymus; MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation 60,770 full-length cDNAs."; Nature 420:563-673(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=NOD; TISSUE=Thymus; MEDIATION OF 1101/GT.152600; MEDIATRE=26350913; PubMed=11076861; DOI=10.1101/GT.152600; MEDIATRE=26350913; PubMed=11076861; DOI=10.1101/GT.152600; Shibata K., Itoh M., Airawa K., Kiteunai T., Tashiro H., Itoh M., Suni N., Ishli Y., Nakamura S., Hazama M., Nishina T., Harada A., Sumannoto R., Mateumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yonamatsu M., Inoue Y., Kira A., Hayashizaki Y., Rawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; "RIKEN integrated sequence analysis (RISA) system-384-format
                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RIKEN FANTOM Consortium; "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=NOD; TISSUE=Thymus;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                  319 AA.
                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                 PRT;
                                                                                                                                       STRAIN=NOD; TISSUE=Thymus;
The FANTOM Consortium,
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                                                                                                                          300 VCRAQTMSNSGIK 312
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                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse)
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119
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                                                                                                                                                  Carninci P.,
                                                                                                                                         Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., Fukuda S., Furuno M., Hanagaki T., Haraoka T., Hirozan T., Hiramcko K., Kagawa I., Kosukawa T., Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya & Kurihara C., Mateuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki A., Murata M., Nakamura M., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H., Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T., Tomaru A., Toya T., Yasunishi A., Muramateu M., Hayashizaki Y., Subhitted (Apr. 2002) to the EMBL/GenBank/DDBJ databases.
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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multicapillary sequencer.";
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Last annotation update)
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Best Local Similarity 85.3%; Pred. No. 1.5e-69;
Matches 267; Conservative 15; Mismatches 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MGD; MGI:102774; Scyel.
G0; G0:0003576; F: nucleic acid binding; IEA.
G0; G0:0000049; F: FRNA binding; IEA.
InterPro; IPR008994; Nucleic acid OB.
InterPro; IPR002894; TRNA bind.
PEam; PF01588; TRNA bind.
PROSITE; PS50886; TRNA bind.
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Xenopus laevis (African clawed frog)
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   sequencing pipeline with 384 m
Genome Res. 10:1757-1771(2000)
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HSSP; Q12904; 1EUJ.
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                                                                                          SEQUENCE FROM N.A.
STRAIN=NOD; TISSUE=Thymus;
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RESULT 6

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Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
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Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.P., Casvant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toobhyuki S., Carninci P., Frange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Rosak S.A., McKennan D.J., McKernan R.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Sanchez A.,
Krzywinski M.I., Skalska U., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Gobersation and initial analysis of more than 15,000 full-length human
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MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC046580; AAH46580.1; -.
HSSP; Q12904; 1FL0.
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6e-55;
47; J
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GO; GO:0000049; F:tRNA binding; IEA.
INTERPRO! FRO008292; EMAPII.
INTERPRO! IPR008994; Nucleic acid OB.
INTERPRO! IPR002547; TRNA bind.
PHEN; PIRSPO05581; EMAPI!; 1.
PROSITE; PS50886; TRBD; 1.
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                                                                                                                                                                                                                                                                                                                                                                       and mouse cDNA sequences."
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REMEDINGE FOR WAY N.A.

REDEINNE-20196006; PubMed=10731112; DOI=10.1126/science.287.5461.2185;

RADAGENER FOR SCHOKER S.E., Holt R.A., Farans C.A., Gocayne J.D.,

RADAGENER A., Lewis S.E., Richards S., Amburner M., Henderson S.N.,

Sutcon G.G., Wortnam J.R., Yandell M.D., Zhang Q., Chen L.K.,

RADAGEN R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeitfer B.D.,

RADAGEN R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeitfer B.D.,

RADAGEN R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeitfer B.D.,

RADAGEN R.C., Rogers Y.W., Blazej R.G., Champe M., Pfeitfer B.D.,

RADAGEN R.M., Baun B.P., Barder B.G., Ralson C.R., Gabor G.L.,

RADAGEN R.M., Benns P.V., Bernam B.P., Bandari D., Bollankov S.,

RADAGEN R.M., Borler M.R., Bouck J., Bayraktaroglu L., Beasley E.M.,

Borkova D., Botchen M.R., Bouck J., Brokstein P., Brottier P.,

RADAGON K., Doup L.E., Downes M., Dugan-Rocha S., Fleischmann W.,

RADAGON K., Doup L.E., Downes M., Dugan-Rocha S., Fleischmann W.,

RADAGON K., Doup L.E., Downes M., Dugan-Rocha S., Fleischmann W.,

RADAGON K., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,

RADAGEN G., Gong F., Gorrell J.H., Gu Z., Glabart W.M., Gabrielian A.E.,

RADAGEN D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,

RADAGEN D., Lei Y., Levitsky A.A., Li J.J., Li Z., Liang Y., Lin X.,

Liasko P., Lei Y., Levitsky A.A., Li J.J., Li Z., Liang Y., Lin X.,

RADAGEN D., Mollahian N.V., Mobarriy C., Morris J., Mochresi A.,

RADAGEN D., Mollahian N.K., Nixon K., Nusmy D.M., Nelson D.L.,

RADAGEN D., Mollahian N.K., Nixon K., Nusmy D.M., Nelson D.K.,

RADAGEN D., Rei Y. Tector C., Turner R., Vonter S., Wang A.H., Wang X.,

RADAGEN D., Rei Y. Remington K., Sampler R., Wang A.H., Wang X., Wang A.Y., Wang R.Y., Wassarman D.A., Weinstond M., Strong R., Sahe H.,

RADAGEN D.K., Worker R., Wong R., Wang S., Yao O.A., Ye J.,

RADAGEN D.K., Wassarman D.A., Weinstond R., Zhong K., Zhong K., Zhong W., Zhong W., Zhong X., Rang C., Shend W., Wassarman D.A., Weinstond R., Shue B.C., Shong Y., Wassarman D.A., Weinstond R., Shue B., Sh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cenlker S. B., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Pacleb J.M., Park S., Pfeifer B.D., Richards S., Sodergren E.J., Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C., Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.; Finishing a whole-genome shotgun: Release 3 of the Drosophila melanogaster euchromatic genome sequence.";
                                                                                                                                                      Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Haxapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
                                                                         Last sequence update)
Last annotation update)
             323 AA
                                                         Created)
             PRT;
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MEDLINE=22426065; PubMed=12537568;
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                                                      01-MAY-2000 (TrEMBLrel. 13, 01-OCT-2002 (TrEMBLrel. 22, 01-MAR-2004 (TrEMBLrel. 26,
             PRELIMINARY;
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SEQUENCE FROM N.A.
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                                                                                                                                               ORFNames=CG8235;
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                  Q9V504
Q9V504
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SYM_CAEEL
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LIQAEIQNGVKQIAFP-----SGTPLHANSMVSENVIQSTAVTTVSSGTKEQIKGGTG 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 AVLKRLEQKGAEADQIIEYLKQQVSLLKEKAILQATLREEKKLRVENAKLKKEIEELKQE 65
Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R., Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E.; "The transposable elements of the Drosophila melanogaster euchromatin:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                        SEQUENCE FROM N.A.

MEDLINE=22426669; PubMed=12537572;

Mista S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,

Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,

Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P.

Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,

Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,

Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28;
                                                                                                                                                                                                                                                                                                                                                                   Annotation of the Drosophila melanogaster euchromatic genome:
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EMBL, AE003835; AAF59019.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to the EMBL/GenBank/DDBJ databases
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44.9%; Pred. No. 4.4e-31;
tive 57; Mismatches 88;
                                                                                             a genomics perspective.";
Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
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IntAct; Q9V504; -.
FlyBase; Fsgn003335; CG8235.
GO: GO:000576; F:nucleic acid binding; IEA.
GO: GO: PR008932; EMAPII.
InterPro; IPR008934; Nucleic acid OB.
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Pfam; PF01588; tRNA_bind; 1.
PIREF; PIRSF005381; EMAPII; 1.
PROSITE; PS50886; TRBD; 1.
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Matches 141, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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351 AA

PRT;

PRELIMINARY;

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238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68 QABIQNGVKQIAPPSGTPLHANS----MVSENVIQSTAVTTVSSGTKEQ----IKGGTGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Caenorhabditis elegans.
Bukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                       Anopheles gambiae str. PEST.
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta; Pterygota;
Neoptera; Endopterrygota, Diptera; Nematocera; Culicoidea; Anopheles.
NCBI_TaxID=180454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-OCT-2004 (Rel. 45, Last annotation update)
Methionyl-tRNA synthetase (EC 6.1.1.10) (Methionine--tRNA ligase)
                                                                                                                                                                                                                                                                                                                            Anopheles Genome Sequencing Consortium;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33;
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01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
AgCP11872 (Fragment).
Name=agCG47516; ORFNames=ENSANGG0000014444;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39.8%; Score 625.5; DB 2; 42.7%; Pred. No. 2e-28; tive 53; Mismatches 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP; Q12904; IEUU.
GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0000049; F:tRNA binding; IEA.
INCEPPO; IPR008932; EMAPII.
INCEPPO; IPR00894; Nucleic acid OB.
INCEPPO; IPR00894; Nucleic acid OB.
INCEPPO; IPR00894; Nucleic acid OB.
FRANF, PROSSB9; ENNA bind.
PROSITE; PSSS086; TRBD; 1.
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Matches 134; Conservative 53; Mismatches
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15-DEC-1998 (Rel. 37, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                  preliminary data.
EMBL; AAAB01008933; EAA09959.1;
HSSP; Q12904; 1EUJ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             299 GVCRAQTMSNSGIK 312
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GPVKAQTLKNVQVK 351
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                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN=PEST;
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839 DKVEIMEVPADSKPGTPVVCPPYTHRPDEQLNPKKKIWETVAEDLKVSAEGFAEWKGQPL 898
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Matches 117;
                                                                                                                                                                          ORYSA
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                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified ann-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EELKQELIQAEIQNGVKQIAFP--SGTPLHANSMVSENVIQSTAVTTVSSGTKEQIKGGT 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          174 LYVEEVDVGEIAPRTVVSGLVNHVPLEQMQNRMVILLCNLKPAKMRGVLSQAMVMCASSP 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MANNDAVLKRLEQKGAEADQII-EYLKQQVSLLKBKAILQATLREEKKLRVENAKLKKEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      118 GDEKKAKEKIEKKGEKKEKKQQSIAGSADSKP----IDVSRLDLRIGCIITARKHPDADS
                                                                                                                                                                          -i - CATALYTIC ACTIVITY: ATP + L-methionine + tRNA(Met) = AMP + diphosphate + L-methionyl-tRNA(Met) .

-i - SUBCELLULAR LOCATION: Cytoplasmic (By similarity) .

-i - SIMILARITY: Belongs to the class-I aminoacyl-tRNA synthetase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35.9%; Score 564; DB 1; Length 917; 42.3%; Pred. No. 2.1e-24;
                                                                                                    The C. elegans sequencing consortium;
Genome sequence of the nematode C. elegans: a platform for
investigating biology.";
Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42.3%; Pred. No. 2.15-27,
Live 52; Mismatches 100; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .917 AA; 101713 MW; 3842AABA314FBDF0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "KMSKS" region.
ATP (By similarity).
                                                                                                                                                                                                                                                         family.
SIMILARITY: Contains 1 tRNA-binding domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "HIGH" region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tRNA-binding.
                                                               STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; Z73427; CAA97803.1; -. PIR; T22898; T22898.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
       NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
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         NAME OF THE PROPERTY OF THE PR
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isp-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                     16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 45, Last annotation update)
25-OCT-2004 (Rel. 45, Last annotation update)
16-OCT-2004 (Rel. 46, Last annotation u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Deniziak M., Mirande M.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
--- CATALYTIC ACTIVITY: ATP + L-methionine + tRNA(Met) = AMP +
diphosphate + L-methionyl-tRNA(Met).
--- SIBCELLULAR LOCATION: Cytoplasmic (Probable).
--- SIMILARITY: Belongs to the class-I aminoacyl-tRNA synthetase
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"KMSKS" region.
ATP (By similarity).
tRNA-binding.
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                                                                                                                                                                                                                                                                                                                                             804 AA.
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PEAM, PF00133, TRNA-synt_1; 1.
PIRSF, PIRSF001528, MetRS dimerising; 1.
PRINTS, PR01041; TRNASYNTHMET.
TIGREAMS; TIGR0398; metG; 1.
PROSITE; PS00178; AA TRNA_LIGASE_1; 1.
PROSITE; PS00186; TRBD; 1.
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InterPro; IPR008994; Nucleic acid OB.
InterPro; IPR002300; FRNA-977t la.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPRU02300; ......f.
InterPro; IPR001412; tRNA-synt_I.
InterPro; IPR002304; tRNA-synt_met.
InterPro; IPR002547; tRNA bind.
InterPro; IPR009080; tRNAByn la_bind.
                                                                                                                                                                                                                                                                                                                                             PRT;
294 EVKGKGVCRAQTMSNSGIK 312
                                                                                             917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF040700; AAC99620.1; -.
                                                                                             899 LIGSESKMTAPTLRGVHVK
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                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP; Q12904; IFLO.
Gramene; Q9ZTS1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=4530;
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                                                                                                                                                                                  TVVSGLVNHVPLEQMQNRMVILLCNLKPAKMRGVLSQAMVMCASSPE--KIEILAPPNGS 245
                                                                                                                                                                                                                                                                246 VPGDRITFDAFPGEPDKELNPKKKIWEQIQPDLHTNDECVATYKGVPFEVKGKGVCRAQT 305
                                                                                                                                                                                                                                                                                         GVKQIAFPSGTPLHANSMVSENVIQSTAVTTVSSGTK--EQIKGGTGDEKKAKEKIEKKG 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TVVSGLVKFIPLEEMQNRKVCVLCNLKPVAMRGIKSHAMVLAASNEDHTKVELVEPPESA
                                                         ------FRNKFAGSQAERSSKAQADAEAKKVADKLKG------TKLSDGG
                                                                                                                          MEDILNE=98184040; PubMed=9523439; DOI=10.1098/rspb.1998.0311; Pahlher S., Krasko A., Schuetze J., Mueller T.M., Mueller W. B.G.; "Isolation and characterisation of the cDNA, encoding a potential morphogen from the marine sponge Geodia cydonium that is conserved in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KMRGVLSQAMVMCASSPEKIEILAPPNGSVPGDRITFDAFPGEPDKELNPKKKIWEQIQP
                                                                                                 EKKEKKOOSIAGSADSK----PIDVSRLDLRIGCIITARKHPDADSLYVEEVDVGEIAPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          157 LRIGCIITARKHPDADSLYVEEVDVGEIAPRTVVSGLVNHVPLEQMQNRMVILLCNLKPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Porifera, Demospongiae; Tetractinomorpha;
Astrophorida; Geodiidae; Geodia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2; Length 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Endothelial-monocyte-activating polypeptide related protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   149 AA; 16499 MW; 61272889BE17C7EF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. R. Soc. Lond', B, Biol. Sci. 265:421-425(1998).
EMBL; Y14947; CAA75164.1; -.
HSSP; Q12904; FLO.
G0; G0:00003576; F:mucleic acid binding; IEA.
G0; G0:0000049; F:tRNA binding; IEA.
InterPro; IPR008994; Nucleic acid_OB.
InterPro; IPR008994; RNA_bind.
Pram; PF01588; tRNA_bind; 1.
PROSITE; PSS0886; TRBD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31.8%; Score 499.5; DB 2 62.2%; Pred. No. 1.4e-21; ive 24; Mismatches 31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             149 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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798 IASGEIR 804
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=6047;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=EMAPR1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92;
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AC 06254
AC 06254
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DT 01-AU DT 01-OU DT 01-OU DT 01-OC DE ENDOR OC DE ENDOR OC DE ENDOR OC DE ENDOR OC AGIO O
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797 AA

PRT;

STANDARD;

SYM\_ARATH

SYM\_ARATH

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the ENML outstation the Buropean Bioinformatics Institute are no restrictions on its use by non-profit institutions as long as its content is in no way
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RAMEDLINES-20083488 PLUMAGE-16017198; DOI-10.101947134.

RAMEDLINES-20083488 PLUMAGE-16017198; DOI-10.101947134.

RAMEDLINES-20083488 PLUMAGE-16017198; DOI-10.1019478.

RAMEDLINES R. Manorge W. Brandt P. Marche R., Mueller M., Reicher B., Mache R., Mueller M., Rechart B., Portetelle D., Perza-Alons M., Schmidtheinn T., Rachert B., Portetelle D., Perza-Alons M., Schmidtheinn T., Rachert B., Portetelle D., Perza-Alons M., Boutry M., Bancoft I., Langham S.-A., McCullagh B., Bilham L., Robben J., Van den Bare R., Dangham S.-A., McCullagh B., Bilham L., Robben J., Van den Baele H., Branken M., Weitjens I., Standarder M., Linkse W., Mooijman P., Klein Lankhorst R., Rose M., Landarcel R., Defoor E., Mooijman P., Klein Lankhorst R., Rose M., Landarcel R., Defoor E., Mooijman P., Klein Lankhorst R., Rose M., Landarcel R., Defoor E., Mooijman P., Klein Lankhorst R., Rose M., Landarcel R., Defoor E., Mooijman P., Klein Lankhorst R., Rose M., Landarcel R., Defoor E., Mooijman P., Klein Lankhorst R., Rose M., Landarcel R., Defoor E., Rose M., Landarcel R., Defoor E., Rose M., Landarcel R., Defoor E., Rose M., Landarcel R., Macher S., Clark L., Dogget J., Hall S., Kay M., Lennard N., McLay J., Perlber R., Borkova D., Bloccker H., Schrief M., Carlum M., McLay J., Tavandi E., Amastre C., Puchal M., Marzee A.C., Schaefer M., Mubourg S., Ramen D., Hiller R., Schmidt W., Lecharry A., Adbourg S., Chefdor F., Cooke R., Berger C., Monfort A., Casacuberta B., Schmall S., Hiller R., Schmidt W., Lecharry A., Adbourg S., Racheller R., Schmidt W., Lecharry A., Adbourg S., Racheller R., Schmidt W., Lecharry A., Adbourg S., Racheller D., Monfort A., Schmed J., Schmidt W., Lecharry A., Berger C., Monfort A., Schmidt W., Lecharry A., Schmidt W., Lecharry A., Berger C., Monfort A., Schmidt W., Berchelle P., Courle R., Marci E., Carola R., Muller R., Schmidt W., Lechar S., France S., France S., Ramer J., Pulton L., Mardis E., Dante M., Pepin K., Gibmen J., Sheet P., Corke R., Huang E., M
                                                                                                                                               ligase) (MetRS).
OrderedLocusNames=At4g13780; ORFNames=F18A5.170;
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                     (Methionine--tRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- CATALYTIC ACTIVITY: ATP + L-methionine + tRNA(Met) = AMP + diphosphare + L-methionyl-tRNA(Met) -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
-!- SIMILARITY: Belongs to the class-I aminoacyl-tRNA synthetase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-cv. Columbia;
MEDLINE-20083488; PubMed=10617198; DOI=10.1038/47134;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
25-OCT-2004 (Rel. 45, Last amotation update)
Probable methionyl-tRNA synthetase (EC 6.1.1.10)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: Contains 1 tRNA-binding domain.
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EMBL; AY398430; AAQ97863.1; -.
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and for commercial
  removed. Usage by and for commercial ont (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PNGSVPGDRITFDAFPGEPDKELNPKKKIWEQIQPDLHTNDECVATYKGVPFEVKGKGVC 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUENCE FROM N.A.

TISSUE-Kidney marrow;
Song H.D., Wu X.Y., Sun X.J., Zhou Y., Liu T.X., Deng M., Zhang G.W.,
Shong Y., Chen Y., Kuan Z., Jiang C.L., Fan H.Y., Zon L.I.,
Shenki J.P., Look A.T., Chen Z.;
Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Aminoacyl-tRNA synthetase; ATP-binding; Ligase; Protein biosynthesis; RNA-binding; tRNA-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name-yars; Synonyma-YMRS;
Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26 36 "HIGH" region.
348 352 "KMSKS" region.
351 351 ATP (By similarity).
635 738 tRNA-binding.
797 AA; 89853 MW; BOF523C2E0C1017F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Tyrosyl-tRNA syntherase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31.7%; Score 499; DB 1;
52.9%; Pred. No. 1e-20;
iive 31; Mismatches 51.
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                                                                                                                                                                                          InterPro; IPR008224; MetRS_dimerising.
InterPro; IPR008994; Nucleic_acid_OB.
InterPro; IPR001809; IRNA-synt_1a.
InterPro; IPR001112; IRNA-synt_1a.
InterPro; IPR001112; IRNA-synt_interPro; IPR002104; IRNA-synt_met.
InterPro; IPR002547; IRNA-synt_met.
InterPro; IPR002547; IRNA-synt_interPro; IPR00113; IRNA-synt_interPro; IPR001013; IRNA-synt_interPro; IPR001013; IRNA-synt_interPro; IPR001013; IRNA-synt_interPro; IPR010013; IRNA-synt_interPro; IPR010013; IRNA-synt_interPro; IPR010013; IRNA-synt_interPro; IPR010013; IRNA-synt_interPro; IPR010013; IRNA-SYNTHMET.
INGRRAMS; ITGR00399; metCi
                      entities requires a license agreement ((or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
  and this statement is not
                                                                                      EMBL, AL035528; CAB36842.1; --
EMBL, AL161337; CAB78420.1; --
PIR, T05247, T05247
HSSP, Q12904; 1E7Z.
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                                                                                                                                                                             GeneFarm; 2798;
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SEQUENCE
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Q6TGS6
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-KKQQSIA-----GSADSKP----IDVSRLDLRIGCIITARKHPDADSLYVEE 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             179 VDVGEIAPRTVVSGLVNHVPLEQMQNRMVILLCNLKPAKMRGVLSQAMVMCAS---SPEK 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 393 IDVGEEQPRTVVSGLVAYITEEQLQDRLVVLLCNLKPQKMRGIBSQAMVLCASIBGEPRK 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                236 IEILAPPNGSVPGDRITFDAF-PGEPDKELNPKKKIWEQIQPDLHTNDECVATYKGVPFE 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EESKIDILIDKNQDVKKKLKKAFCEPGNVE-NNGVLSFVKHVLF----PLHSEFVIKRDPK 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   283 FGGDKVYTDFEEVEKDFAA-----EQIH--PGDLKASVELALNKLLDPIRKKFESPE 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----ENVIQSTAVTTVSSGTKEQIKGGTGDEK-----KAKEKIEKKGEKKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44 EEKKLRV---ENAKLKKEIEELKOELIQAEIONG----VKQIAFPSGTPLHANSMVS----
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Whole;
MEDLINE=22188257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 28.8%; Score 453.5; DB 2; Length 529; Best Local Similarity 39.8%; Pred. No. 2.7e-18; Matches 123; Conservative 43; Mismatches 78; Indels 65
ZETN; ZDB-GENE 30425-25; Yars.

ZETN; ZDB-GENE 30425-25; Yars.

GO; GO:000356; F:ATP binding; IEA.

GO; GO:0000367; F:ERNA binding; IEA.

GO; GO:00004831; F:tyrosine-tRNA ligase activity; IEA.

GO; GO:0006431; F:tyrosine-tRNA ligase activity; IEA.

GO; GO:0006431; F:tyrosine-tRNA aminoacylation; IEA.

GINTE-PRO; IPRO08202; ERAPHI.

INTE-PRO; IPRO08202; ERAPHI.

INTE-PRO; IPRO02307; Tyr_ERNA-synt_lb.

R PÉAN; PFO0579; ERNA-synt_lb.

R PÉAN; PFO1588; ERNA bind; lb.

R PERS; PRSF005381; ERNA bind; l.

R PERS; PRSF005381; ERNA bind; l.

R PERS; PRSF00534; trys; l.

R PROSTTE; PSG866; TRBS; l.

R PROSTTE; PSG866; TRBS; l.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      529 AA; 59505 MW; C3314003813B9336 CRC64;
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              295 VK-GKGVCR 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 513 TKLGRITCK 521
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Bovinae; Bos
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Loca
Matches
     -----ENVIQSTAVTTVSSGTKEQIKGGTGDEK-----KAKEKIEKKGEKKE 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----KKQQSIAG----SADSKPIDVSRLDLRIGCIITARKHPDADSLYVEE 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     333 LKKLTSSAYPEPSKNKGGVKGNPKQTTDDDEVIPSRLDIRVGKVISVEKHPDADSLYLEK 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VDVGEIAPRTVVSGLVNHVPLEQMQNRMVILLCNLKPAKMRGVLSQAMVMCAS---SPEK 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         283 FGGDKVYTDFEEVEKDFÅA-----EQIH--PGDLKASVELALNKLLDPIRKKFESPE 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              236 IEILAPPNGSVPGDRITFDAF-PGEPDKELNPKKKIWEQIQPDLHTNDECVATYKGVPFE 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44 EEKKLRV--ENAKLKKEIEELKQELIQAEIQNG----VKQIAFPSGTPLHANSMVS---- 93
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano, N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Schwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2; Length 529;
                                                                                                                                                                                                                                       A Straubberg R.;
Lybmitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
Lybmitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
R GO; GO:0005224; RAH76589.1; ...
R GO; GO:000049; F:ATP binding; IEA.
GO; GO:000049; F:RNA binding; IEA.
GO; GO:000049; F:RNA binding; IEA.
R GO; GO:000491; F:tyrosine-ENA ligase activity; IEA.
R GO; GO:0004937; P:tyrosine-ENA aminoacylation; IEA.
R InterPro; IPR008223; EMAPLI.
R InterPro; IPR008236; RNA-synt_lb.
R InterPro; IPR002305; TRNA-synt_lb.
R InterPro; IPR002307; TYE ENNA-synt_lb.
R EAM; PPO1589; LRNA-synt_lb; 1.
R Fam; PPO1589; RNA-synt_lb; 1.
R Fam; PR01589; LRNA-synt_lb; 1.
R FIRSF; PIRSF006391; EMAPLI: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28.7%; Score 451.5; DB 2; Length 5: 38.5%; Pred. No. 3.5e-18; ive 46; Mismatches 79; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Aminoacyl-tRNA synthetase.
SEOUENCE 529 AA; 59533 MW; A3264E3E39D362F4 CRC64;
                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             527 AA.
                                                                                                                                                                             and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 38.5
Matches 119; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PS50886; TRBD
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                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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SYYC BOVIN
ID SYYC BOVIN
AC Q29465; Q9TSJ1;
                                                                                                                                                                                                                                  TISSUE=Whole;
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                                                                                                                                                                                                                                                                  Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matsuka G.K.H., Maidenov V.G., Odynets K.A., Woodmaska M.I., Matsuka G.K.H., Wientjes F.-J., Gassen H.G., Kornelyuk A.I.; Matsuka G.K.H., Wientjes F.-J., Gassen H.G., Kornelyuk A.I.; Mamino acid sequence of bovine tyrosyl-FRNA synthetase. Possible generation of the isolated cytokine-like C-terminal domain via proteolytic cleavage at the 'PEST'-like sequence."; Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
01-NOV-1997 (Rel. 45, Last sequence update)
25-OCT-2004 (Rel. 45, Last sequence update)
25-JAN-2005 (Rel. 46, Last annotation update)
Tyrosyl-tRNA synthetase, cytoplasmic (EC 6.1.1.1) (Tyrosyl-tRNA Name-YRAS; Synonyms-TYRS;
Bos taurus (Bovine)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                diphosphate + L-tyrosyl-tRNA(Tyr).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: Belongs to the class-I aminoacyl-tRNA synthetase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Liver;
Kornelyuk A.I., Levanets O.V., Naidenov V.G., Woodmaska M.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Acetylation; Aminoacyl-tRNA synthetase; ATP-binding; Ligase; Protein biosynthesis; RNA-binding; tRNA-binding.

INIT MET 0 0 By similarity.

MOD_RES 1 1 N-acetylglycine (By similarity).

SITE 221 225 "KNGKS" region.

DOMAIN 363 467 tRNA-binding.

CONFLICT 20 V -> P (in Ref. 2).

CONFLICT 20 1 201 L -> P (in Ref. 2).

SEQUENCE 527 AA; 59018 MW; E3F66789F75EA7D8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     / Match 28.6%; Score 450; DB 1; Length 527; Local Similarity 36.9%; Pred. No. 4.2e-18; tes 114; Conservative 55; Mismatches 76; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases -1- CATALYTIC ACTIVITY: ATP + L-tyrosine + tRNA(Tyr) = ^{1}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: Contains 1 tRNA-binding domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF01588; tRNA_bind; 1.
PRINTS; PR01040; TRNASVNTHTYR.
TIGREAMS; TIGR00234; tyrS; 1.
TIGREAMS; TIGR00234; tyrS; 1.
PR051TE; PS00178; AA TRNA_LIGASE_I; FALSE_NEG.
PROSITE; PS50886; TRBD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR008994; Nucleic_acid_OB.
InterPro; IPR002305; RNNA-synt_1b.
InterPro; IPR001412; tRNA-synt_I.
InterPro; IPR002547; tRNA_bind_.
InterPro; IPR002547; tRNA_bind.
InterPro; IPR002307; TYT_ERNA-synt_1b.
Pfam; PF00579; tRNA-synt_lb; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF087021; AAC82467.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 16-211 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IISSUE=Liver;
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TISSUE-Bone, and Lung;

WEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

METARUBDER R.D., Felngold E.A., Grouse L.H., Derge J.G.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

And Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Haish F.,

Diatchenco L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

And S.E., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Robar S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Glibs R.A.,

Rabak S.A., Warny D.M., Schergren B.D., Dickson M.C.,

Mating M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Conforman J.W., Marny M.A., Marra M.A.,

Beneration and initial analysis of more than 15,000 full-length human
                                                                                                             132 EKK------EKKQQSIAGSA-DSKPIDV--SRLDLRIGCIITARKHPDADSLYVEEV 179
                                                                                                                                   DVGEIAPRTVVSGLVNHVPLEQMQNRMVILLCNLKPAKMRGVLSQAMVMCASSP---EKI 236
                                                                                                                                                                                                                               --KEKIEKKG 131
                                                                                                                                                                                                                                                                                             EILAPPNGSVPGDRITFDAF-PGEPDKELNPKKKIWEQIQPDLHTNDECVATYKGVPFEV 295
                                                             EFVILRDEKWGGNKTYTAYLDLEKDFADEVV-HPGDLKNSVEVALNKLLDPIREKFNTPA 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIJNE=96133898; PubMed=8552597; DOI=10.1073/pnas.93.1.166; Ribas de Pouplana L., Frugier M., Quinn C.L., Schimmel P.; "Evidence that two present-day components needed for the genetic code appeared after nucleated cells separated from eubacteria."; Proc. Natl. Acad. Sci. U.S.A. 93:166-170(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=97306356; PubMed=9162081; DOI=10.1074/jbc.272.22.14420; Kleeman T.A., Wei D., Simpson K.L., First E.A.; Human tyrosyl-tranA synthetese shares amino acid sequence homology with a putative cytokine."; J. Biol. Chem. 272:14420-14425(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENVI------QSTAVTTVSSGTKEQIKGGTGDEKKA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     527 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                          K-GKGVCRA 303
                                                                                                                                                                                                                                                                                                                                                                                                                                        512 KMGSVSCKS 520
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Direct protein sequencing; Ligase, Protein biosynthesis; RNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PubMed=12477973; DOI=10.1073/pnas.242611799;
Yang X.L., Skene R.J., McRee D.E., Schimmel P.;
"Crystal structure of a human aminoacyl-tRNA synthetase cytokine.";
Proc. Natl. Acad. Sci. US.A. 99:15369-15374(2002).
-!- CATALYTIC ACTIVITY: ATP + L-tyrosine + tRNA(Tyr) = AMP +
diphosphate + L-tyrosyl-tRNA(Tyr).
-!- SUBCELDULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to the class-I aminoacyl-tRNA synthetase
                                                                                                    MEDIINE-22608298; PubMed=12665801; DOI=10.1038/nbt810; Gevaert K., Goethals M., Martens L., Van Damme J., Staes A., Thomas G.R., Vandekerckhove J.; "Exploring proteomes and analyzing protein processing by mass spectrometric identification of sorted N-terminal peptides."; Nat. Biotechnol. 21:566-569(2003).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: Contains 1 tRNA-binding domain.
-!- CAUTION: Ref.1 sequence differs from that shown due to frameshift in position 353.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      X-RAY CRYSTALLOGRAPHY (1.18 ANGSTROMS) OF 3-341.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIGRPAMS; TIGRO0234; tyrS; 1.
PROSITE; PSO0178; AA TRNA_LIGASE_I; FALSE_NEG.
PROSITE; PS50886; TRBD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-acetylglycine.
"HIGH" region.
                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-15, AND ACETYLATION SITE GLY-1.
TISSUE=B-cell lymphoma;
                                                                                                                                                                                                                                                                                                                                                           Bienvenut W.V.;
Unpublished observations (OCT-2004).
[6]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PDB; 1N3L; X-ray; A=1-371.
PDB; 1NTG; X-ray; A/B/C/D=358-527.
PDB; 1Q11; X-ray; A=1-371.
Genew; HGNC:12840; YARS.
H-InvDB; HIX0000381; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U89436; AAB88409.1; -. EMBL; BC001933; AAH01933.1; -. EMBL; BC004151; AAH04151.1; -. EMBL; BC016689; AAH16689.1; -.
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tRNA-binding.
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Proc. Natl. Acad.
                                                                                     rissum=Platelet;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44 EEKKLRVENAKLKKEIEELKQELIQAEIQNG------VKQIAFPSGTPLHANSMVS 93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 28.6%; Score 450; DB 1; Length 527; Best Local Similarity 36.7%; Pred. No. 4.2e-18; Matches 117; Conservative 51; Mismatches 67; Indels 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   339
59012 MW; A7E0E3B84390579B CRC64;
 "KMSKS" region.
tRNA-binding.
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286 ATYKGVPFEVK-GKGVCRA 303
                                              502 AQWKQTNFMTKLGSISCKS 520
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GenCore version 5.1.6
Copyright (c) 1993 -- 2005 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

August 3, 2005, 21:46:39 ; Search time 41 Seconds (without alignments) 732.186 Million cell updates/sec

US-10-623-567A-1 1573 1 MANNDAVLKRLEQKGAEADQ......FEVKGKGVCRAQTMSNSGIK 312 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched: 283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

	Description	riom H	endothelial monocy	hypothetical prote		ARC1 protein - yea	probable methionyl	hypothetical prote	methionyl-tRNA syn	methionine-tRNA li		probable tRNA synt		hypothetical 12.3	methionine-tRNA li	methionyl-tRNA syn	methionine-tRNA li	methionyl-tRNA syn	methionyl-tRNA syn	methionine-tRNA li	methionyl-tRNA syn	methionine-tRNA li	methionyl-tRNA syn	methionine-tRNA li	methionyl-tRNA syn	methionyl-tRNA syn				
	_	B55053	A55053	T22898	T05247	S64113	C84832	T47822	B75074	D71091	SYTWMT	C85968	D91123	G65095	D69431	E72297	A64572	F64457	E71281	E83656	H71867	F82090	C75395	B70173	AI1459	266067	D95091	H97958	0	A97268
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Ouery	Match	98.3	85.4	35.9	31.7	27.3	25.5	21.8	14.2	13.7	13.0	12.6	12.6	12.4	12.1	11.8	11.7	11.6	11.3	11.3	10.8	10.7	10.7	10.7	10.1	10.0	6.6	6.6	9.9	9.6
	Score	1546	1343	564	499	429	400.5	343	223.5	216	205	198.5	198.5	194.5	191	185.5	183.5	182.5	178.5	177	170	168.5	168.5	168	159.5	LΩ	156.5	156.5	155.5	151
Regult	No.	1	7	٣	4	S	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

methionine-tRNA 11 CsaA protein PA322	methionine-tRNA li methionine-tRNA li	protein secretion methionine-tRNA li	methionine-tRNA li	methionine-tRNA li	methionine-tRNA li	methionyl-tRNA syn	methionine tRNA sy	methionine tRNA sy	methionyl-tRNA syn	methionine-tRNA li	hypothetical prote	methionine-tRNA sy
G69177 A83243	S16682 F70338	H72655 T64113	AH0776	H86723	F81356	C83210	C85839	H90993	D82249	SYECMT	T23451	C84192
0.0	20	100	~	~	~	N	~	~	~		7	7
651	111	117	677	662	628	677	677	677	731	677	276	689
9.5	9.5	. 6 6	. 6	9.8	9.8	8.6	8.5	8.5	8.5	8.4	8.3	8.3
149	144	141.5	139.5	135	134.5	134.5	133	133	133	132.5	130	129.5
30	32	. e. e.	36	37	38	39	40	41	42	43	44	45

# ALIGNMENTS

RESULT 1 B55053 endothelial monocyte-activating protein II precursor - human C;Species Homo sapiens (man) C;Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 09-Dec-2002
C,Accession: D33033 R,Rouck K.; Fan, Y.; Haehnel, I.; Libutti, S.K.; Kayton, M.L.; Grikscheit, T.; T. G.G., D. M.
7. 3. Biol. Chem. 269, 25106-25119, 1994 A.Title: Characterization of a novel tumor-derived cytokine. Endothelial-monocyte activa A.Reference number: A55053; MUID:95014290; PMID:7929199
A;Accession: B55053 A;Status: preliminary A;Molecule type: mRNA
A,Residues: 1-310 <kao> A;Cross-references: GB:U10117 C;Superfamily: endothellal monocyte-activating polypeptide II precursor (pro-EMAP II)</kao>

	1;	09
	Gaps	LKKEIE
	5;	NAK
310	_	CLRV.
98.3%; Score 1546; DB 2; Length 310;	Pred. No. 1.9e-8/; 0; Mismatches 1; Indels 2; Gaps	1 MANNDAVLKRIEQKGAEADQIIEYLKQQVSLLKEKAILQATLREEKKLRVENAKLKKEIE 60
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98	tive	EOKG
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4,	Best Local Similarity 99.0%; Matches 309; Conservative	1 MA
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Query Match	st L	
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à	-	MANNDAVLKRIEQKGAEADQIIEYLKQVSLLKEKAILQATLREEKKLRVENAKLKKEIE 6	09
Db	1	MANNDAVLKRLEQKGAEADQIIEYLKQQVSLLKEKAILQATLREEKKLRVENAKLKKEIE 6	09
ò	61	ELKQELIQAEIQNGVKQIAFPSGTPLHANSMVSENVIQSTAVTTVSSGTKEQIKGGTGDE	120
Dp	61	ELKQELIQAEIQNGVKQIRFPSGTPLHANSMVSENVIQSTAVTTVSSGTKEQIKGGDE	118
ò	121	KKAKEKI EKKGEKKEKKQQSI AGSADSKPI DVSRLDLRI GCI ITARKHPDADSLYVEEVD	180
Ωp	119	KKAKEKIEKKGEKKEKKOOSIAGSADSKPIDVSRLDLRIGCIITARKHPDADSLYVEEVD	178
ò	181	VGELAPRTVVSGLVNHVPLEQMQNRMVILLCNLKPARMRGVLSQAMVMCASSPEKIEILA	240
ΩÞ	179	VGETAPRTVVSGLVNHVPLEQMQNRMVILLCNLKPAKNRGVLSQAMVMCASSPEKIEILA	238
λ̈́o	241	PPNGSVPGDRITFDAFPGEPDKELNPKKKIWEQIQPDLHTNDECVATYKGVPFEVKGKGV	300
Ωp	239	PPNGSVPGDRITFDAFPGEPDKELNPKKKIWEQIQPDLHTNDECVATYKGVPFEVKGKGV	298
ò	301	CRAQTMSNSGIK 312	
д	299	CRACTMSNSGIK 310	

RESULT 2

A55053
endochbalial monocyte-activating protein II precursor - mouse
crispecies: Mus musculus (house mouse)
C;Species: 08-Jul-1995 #sequence\_revision 03-Aug-1995 #text\_change 09-Jul-2004

Gaps

32;

Indels

677 117 173

-----TPTSTPASGIITE----

233

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A;Map position: 4
A;Introns: 40/1; 88/2; 139/3; 191/3; 268/3; 316/3; 347/1; 382/3; 423/1; 460/3; 482/3; 52*
A;Note: F18A5.170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     668 GEIRTVVSGLVKYIPLEEMQNRMVCVLCNLKPAKMRDIVSQAMVLAASSSDGSKVELVEP 727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PNGSVPGDRITFDAFPGEPDKELNPKKKIWEQIQPDLHTNDECVATYKGVPFEVKGKGVC 301
                                                                                                                                                                                                                                                                                                                                                                                                                            124 KEKIEKKGEKKEKKQQSIAGSADSKPIDVSRLDLRIGCIITARKHPDADSLYVEEVDVGE 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KOKASSKGGGKPKPO----PAADREITMARLDIRVGKIVKAEKHPKADALYVEEIDVGG 667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     234 EKIEILAPPNGSVPGDRITFDAFPGEPDKELNPKKKIWEQIQPDLHTNDECVATYKGVPF 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999.#text_change 09-Jul-2004
                                                                                                                                                   779 LYVEQIDVGESAPRTVVSGLVRHVPLDQMQNRLVVVLCNLKPAKMRGVESRAMVMCASSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          184 IAPRIVVSGLVNHVPLEQMQNRMVILLCNLKPAKMRGVLSQAMVMCASSPE--KIEILAP
                                                                                                                                                                                                                                            EELKQELIQAEIQNGVKQIAFP--SGTPLHANSMVSENVIQSTAVTTVSSGTKEQIKGGT
                                                                                                                                                                                                                                                                                                                                                                                        118 GDEKKAKEKIEKKGEKKEKKQOSIAGSADSKP----IDVSRLDLRIGCIITARKHPDADS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LYVEEVDVGEIAPRTVVSGLVNHVPLEQMQNRMVILLCNLKPAKMRGVLSQAMVMCASSP
                                                                                                        1 MANNDAVLKRLEQKGAEADQII-EYLKQQVSLLKEKAILQATLREEKKLRVENAKLKKEI
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N;Alternate names: G4P1 protein; protein G3085; protein YGL105w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      methionine-tRNA ligase homolog F18A5.170 - Arabidopsis thaliana
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Best Local Similarity 52.9%; Pred. No. 4.8e-23;
Matches 101; Conservative 31; Mismatches 51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Accession: T05247
R;Bevan, M.; Weber, N.; Grueninger, D.; Schmidheini, T.; Bubmitted to the Protein Sequence Database, February 1999
A;Reference number: Z15405
A;Accession: T05247
A;Molecule type: DNA
A;Residues: 1-797 - SBEV
A;Cross-references: UNIRROT: 09SVNS; EMBL: AL035528
A;Experimental source: cultivar Columbia; BAC clone F18A5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C, Superfamily: methionyl-tRNA synthetase, dimer-forming
       Local Similarity 42.3%; Pred. No. 6e-27; ne 135; Conservative 52; Mismatches 100;
                                                                                                                                                                                                                                                                                              294 EVKGKGVCRAQTMSNSGIK 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LIGSESKMTAPTLRGVHVK 917
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KVSSISNGTIR 797
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T22B98
R;Harris, B.
submitted to the EMBL Data Library, May 1996
A;Reference number: 219633
A;Accession: T22B98
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-917 «WIL.>
A;Cross-references: UNIPROT:Q20970; EMBL:Z73427; PIDN:CAA97803.1; GSPDB:GN00022; CESP:F5
A;Accession: 4
A;Gene: CESP:F5BB3.5
A;Gene: CESP:F5BB3.5
A;Agene: CESP:F5BB3.5
A;Agene: CSP:F5BB3.5
A;Agene: CSP:F5B
                                                                                                                                                                                                                                                                                    A; Wolecule type: mRNA
A; Residues: 1-310 < KAO.
A; Residues: 1-310 < KAO.
A; Residues: 1-310 < KAO.
A; Cross-references: UNIPROT: P31230; GB:U10118; NID:g498911; PIDN:AAA62203.1; PID:g498912
B; KAO., J.; Ryan, J.; Brett, G.; Chen, J.; Shen, H.; Fan, Y.G.; Godman, G.; Familletti, F
J. Biol. Chem. 267, 20239-20247, 1992
A; Title: Endothelial monocyte-activating polypeptide II. A novel tumor-derived polypepti
A; Reference number: A44032
A; Molecule type: protein
A; Residues: 145-158, X., 160-164 < KA2.>
A; Residues: 145-158, X., 160-164 < KA2.>
A; Experimental source: methylcholanthrene A fibrosarcoma cells
A; Note: sequence extracted from NCBI backbone (NCBIP:115676)
C; Superfamily: endothelial monocyte-activating polypeptide II precursor (pro-EMAP II)
                                                                    J. Biol. Chem. 269, 25106-25119, 1994
A; Title: Characterization of a novel tumor-derived cytokine. Endothelial-monocyte activa A; Reference number: A55053; MUID:95014290; PMID:7929199
                                              Ŀ.
C;Accession: A55053; A44032
R;Kao, J.; Houck, K.; Fan, Y.; Haehnel, I.; Libutti, S.K.; Kayton, M.L.; Grikscheit,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ELKQELIQAEIQNGVKQIAFPSGTPLHANSMVSENVIQSTAV-TTVSSGTKEQIKGGTGD 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120 EKKAKEKIEKKGEKKEKKQQSIAGSADSKPIDVSRLDLRIGCIITARKHPDADSLYVEEV 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DVGEIAPRTVVSGLVNHVPLEQMQNRMVILLCNLKPAKMRGVLSQAMVMCASSPEKIEIL 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            240 APPNGSVPGDRITFDAFPGEPDKELNPKKKIWEQIQPDLHTNDECVATYKGVPFEVKGKG 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          238 APPNGSVPGDRITFDAFPGEPDKELNPKKKIWEQIQPDLHTNAECVATYKGAPFEVKGKG 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ELKÓELILAEIHNGVEÓVRVRLSTPLOTNCTASESVVOSPSVATTASPATKEQIK--AGE 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MANNDAVLKRLEQKGAEADQIIEYLKQQVSLLKEKAILQATLREEKKLRVENAKLKKEIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85.4%; Score 1343; DB 2; Length 3
85.9%; Pred. No. 4.7e-75;
ive 13; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 85.9$
Matches 269; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    300 VCRAQTMSNSGIK 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VCRAQTMANSGIK 310
                                                                                                                                                                                                                                                       A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180
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Bancroft, I.; Mewes, H.W.; Mayer

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Gaps

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Length 797;

241

DB 2; Length 917;

35.9%; Score 564;

Match

Query

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(pro-EMAP

9

226

261

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hypothetical protein F24G16.250 - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) (Species: Arabidopsis thaliana (mouse-ear cress) (Species: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 17-Feb-2003 (Speciession: T47822 (Speciession: T47822 (Speciession: T4782) (Modesto, D.; Pigazzi, M.; Valle, G.; Mewes, H.W.; Lemcke, K.; submitted to the Protein Sequence Database, February 2000 (A) Reference number: 224477
                                                                                                   A;Residues: 1-440 <STO>
A;Cross-references: UNIPROT:Q7XJM9; GB:AE002093; NID:g4895232; PIDN:AAD32818.1; GSPDB:GN
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Superfamily: endothelial monocyte-activating polypeptide II precursor (pro-EMAP II)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            135 EKKQQSIAGSADSKP----IDVSRLDLRIGCIITARKHPDADSLYVEEVDVGEIAPRT 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            262 EKKK-----PAEPEPAKKEAELSVSLLNIQVGLIRKAWKHPSADSLLVBEIDVGEDKVRQ 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VVSGLVNHVPLEQMQNRMVILLCNLKPAKMRGVLSQAMVMCASSPEK--IBILAPPNGSV 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VKQIAPPSGTPLHANSMVSENVIQSTAVTTVSSGTKEQIKGGTGDEKKAKEKIEKKGEKK 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                    101 AVTTVSSGTKEQIKGGTGDEKKAKEKIEKKGEKKEKKQQSIAGSADSKPIDVSRLDLRIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          161 CIITARKHPDADSLYVEEVDVGEIAPRTVVSGLVNHVPLEQMQNRMVILLCNLKPAKMRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      221 VLSQAMVMCAS--SPEKIEILAPPNGSVPGDRITFDAFPGEPDKELNP----KKK
                                                                                                                                                                                                                                                                                                                                                                                                                    22 IEYLKQQVSLLKEKAILQATLRE-----EKKLRVE-NAKLKKEIEELKQELIQAEIQNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ||:|::| |:|| ||||| |:| |||||| BGERVSFSGIEGKPEDVLNPKKKQLEKITPGLYTDENGVATYKGIQF-MTSAGPC 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         247 PGDRITFDAFPGEPDKELNPKKKIWEQIQPDLHTNDECVATYKGVPFEVKGKGVC 301
                                                                                                                                                                                             A;Gene: At2g40660
A;Map position: 2
C;Superfamily: endothelial monocyte-activating polypeptide II precursor
                                                                                                                                                                                                                                                                                                           Length 440;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 273;
                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: DNA
A;Rebidues: 1-273 < DNA>
A;Cross-references: EMBL:AL138647
A;Experimental source: cultivar Columbia; BAC clone F24G16
A; Reference number: A84420; MUID: 20083487; PMID: 10617197
                                                                                                                                                                                                                                                                                                   Query Match 25.5%; Score 400.5; DB 2; Best Local Similarity 35.6%; Pred. No. 2.5e-17; Matches 105; Conservative 45; Mismatches 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21.8%; Score 343; DB 2;
37.8%; Pred. No. 4.6e-14;
tive 40; Mismatches 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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Matches 84; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Map position: 3
A;Introns: 157/3; 226/3
A;Note: F24G16.250
                             A; Accession: C84832
A; Status: preliminary
A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary
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                                                                                                                                     A,Reference number: S64112
A,Accession: S64113
A,Molecule type: DNA
A,Molecule type: DNA
A,Residues: 1-376 <CAS>
A,Cross-references: UNIPROT:P46672; EMBL:Z72627; NID:g1322647; PIDN:CAA96812.1; PID:g132
A,Experimental source: strain S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probable methionyl-tRNA synthetase [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004

C;Accession: C84832

R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vankken, S.E.; Umayam, L.; Tallon, L.

euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.

Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Title: The yeast protein Arclp binds to tRNA and functions as a cofactor for the methi
A,Reference number: S72274; MUID:97050848; PMID:8895587
                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: DNA
A;Residues: 1-376 <CAM».
A;Cross-treferences: EMBL:X97644; NID:g1310710; PIDN:CAA66247.1; PID:g1310719
R;Simos, G.; Segref, A.; Fasiolo, F.; Hellmuth, K.; Shevchenko, A.; Mann, M.; Hurt, E.C.
EMBO J. 15, 5437-5448, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Description: functions as a cofactor for methionyl- and glutamyl-tRNA synthetases C;Superfamily: endothelial monocyte-activating polypeptide II precursor (pro-EMAP II) C;Keywords: cytosol; homodimer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         è
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       161 HPRGKPDEETLKKLREEAKAKKAAKKAANAKQQQEQQNKAPEKP-KPSAIDFRVGFIQKA 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56 KKEIE---ELKQELIQAEIQNGVKQIAFPSGTPLHANSMVSENVIQSTAVTTVSSGTKEQ 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               113 IKGGTGDE---KKAKEKIE-KKGEKK---EKKQQSIAGSADSKPIDVSRLDLRIGCIITA 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        220 IKHPDADSLYVSTIDVGDEEGPRTVCSGLVKHFPLDAMQERYVVVCNLKPVNMRGIKST 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       225 AMVMCASSPEKIEILAPPNGSVPGDRITFDAFPGE-PDKELNPKKKIWEQIQPDLHTNDE 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    280 AMVLCGSNDDKVEFVEPPKDSKAGDKVFFEGFGDEAPMKQLNPKKKIWEHLQPHFTTNDG 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        166 RKHPDADSLYVEEVDVG-EIAPRTVVSGLVNHVPLEQMQNRMVILLCNLKPAKMRGVLSQ 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:X95481; NID:g1620459; PIDN:CAA64750.1; PID:g1620460
C;Genetics:
  C;Species: Saccharomyces cerevisiae
C;Date: 17-May-1996 #sequence revision 17-May-1996 #text_change 09-Jul-2004
C;Accession: S64113; S69425; $72274
R;Castegnoli, L.; Paoluzi, S.; Minenkova, O.
submitted to the Protein Sequence Database, May 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tch 27.3%; Score 429; DB 2; Length 376; al Similarity 42.7%; Pred. No. 3.7e-19; 105; Conservative 32; Mismatches 81; Indels
                                                                                                                                                                                                                                                                                                         R;Castagnoli, L.; Paoluzi, S.; Minenkova, O. submitted to the EMBL Data Library, April 1996 A;Reference number: S69417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: MIPS:YGL105w; SGD:S0003073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Accession: 872274
A;Status: nucleic acid sequence not shown
A:Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        284 CVATYK 289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-376 <SIM>
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Best Local S:
Matches 105
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7;

40;

160

11;

Gaps

48;

Indels

72;

Length 723;

549

72

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C;Species: Thermus aquaticus
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Dec-2002
C;Datession: A39517
R;Nureki, O.; Muramatsu, T.; Suzuki, K.; Kohda, D.; Matsuzawa, H.; Ohta, T.; Miyazawa, T
J. Biol. Chem. 266, 3268-3277, 1991
A;Title: Methionyl-tRNA synthetase gene from an extreme thermophile, Thermus thermophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:M64273; GB:J05744; NID:g155135; PIDN:AAA27510.1; PID:g155136 A;Experimental source: strain HB8, ATCC 27634 A;Note: the authors translated the codon TAC for residue 323 as Thr C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Superfamily: methionyl-tRNA synthetase, dimer-forming
C;Keywords: aminoacyl-tRNA synthetase; ATP; homodimer; ligase; protein biosynthesis
F;13,19,50,300/Active site: Tyr, His, Asp, Lys #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -EERTVVSGIAKWYRPEELVGKKVVLVANLKPAKLRGIESQGMILAAQEGEAL-ALVTVE 608
                                                                                                                                                                                                                                                                                                                                                                                                                                         550 D--EQIIYFILNYMGRNNPEGA-----KMLLEKYYKREDVIKVA----KEKP----GEESK 595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IAPPSGTPLHANSMVSENVIQSTAVTTVSSGTKEQI-----KGGTGDEKKAKEKIEKKG 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EKKEKKQQSIAGSADSKP-----IDVSRLDLRIGCIITARKHPDADSLYVEEVDVGE 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  184 IAPRTVVSGLVNHVPLEQMQNRMVILLCNLKPAKMRGVLSQAMVMCASSPEKIEILAPPN 243
                                                                                                                                                                                                                                                                                                                                                        73 NGVKQIAF-----PSGTPLHANSMVSENVIQSTAVTTVSSGTKEQIKGGTGDE-- 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---KKAKEKIEKKGEKKEKKQQSIAGSADSKPIDVSRLDLRIGCIITARKHPDADSLYVE 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        178 EVDVGEIAPRTVVSGLVNHVPLEQMQNRMVILLCNLKPAKMRGVLSQAMVMCASSPEKIE 237
                                                                                                                                                                                                                                    20 QIIEYLKQOVSLLKEKAILQATLREEKKLRVENAKLKKEIEBL-----KQELIQAEIQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Reference number: A39517; MUID: 91131636; PMID: 1993699
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; Score 216; DB 2;
; Pred. No. 8.1e-06;
53; Mismatches 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N,Alternate names: methionyl-tRNA synthetase C,Species: Thermus aquaticus
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        13.7%;
29.1%;
        Query Match
Best Local Similarity 29.1%
Matches 71; Conservative
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A; Residues: 1-616 <NUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LLMP 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       238 ILAP 241
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D71091
methiconine-tRNA ligase (EC 6.1.1.10) - Pyrococcus horikoshii
C;Species: D71091
R;Kawarabayasi, Y:; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekir
M; Ohtuku, Y.; Fundhashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi
M; Ohtuku, Y.; Fundhashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi
DNA, Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a
A;Reference number: A71000; MUID:98344137; PMID:9679194
A;Residues: D71091
A;Residues: 1-723 «KAW»
A;Residues: 1-723 «KAW»
A;Residues: 1-723 «KAW»
A;Residues: 1-723 «KAW»
A;Residues: UNIPROT:058721; GB:AP0000004; NID:93236131; PIDN:BAA30090.1; PID:9325
A;Experimental source: strain OT3
A;Note: this accession replaces an interim accession for a sequence replaced by GenBank
C;Genetics:
                                                                                                                                                                                                                                                                                                                                               C;Specide: Pyrococcus abyes:
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
B;Accession: BSD074
B;Accession: Pyrococcus abyesi genome sequence: insights into archaeal chromosome struth. A;Description: Pyrococcus abyesi genome sequence: insights into archaeal chromosome struth. A;Description: Pyrococcus abyesi genome sequence: insights into archaeal chromosome struth. A;Accession: B75074
A;Accession: B7
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                                                                                                                                                                                                                                                                        B75074 methionyl-tRNA synthetase (mets) PAB2364 - Pyrococcus abyssi (strain Orsay)
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larity 29.7%; Pred. No. 2.8e-06;
Conservative 52; Mismatches 75; Indels
             IWEQIQPDLHTNDECVATYKGVPFEVKGKGVCRAQTMSNSGI 311
                                                              || |:: | |:: |
SQGMLLAADDGERVALLMP 711
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nes 77; Conserv
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Best Local S
Matches 77
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10;

Gaps

42;

Indels

89;

Length 616;

3; 210

Gaps

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C; Accession: G65095

E; Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co. S.; Rose, D.G.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997

Science 277, 1453-1462, 1997

A; Title: The complete genome sequence of Escherichia coli K-12.

A; Reference number: A64720; MUID:97426617; PMID:9278503

A; Accession: G65095
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Cipate: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
Cipate: 05-Dec-1997
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Cipate: 06-July Cipate: 07-July Cipa
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A;Cross-references: UNIPROT:028819; GB:AE001003; GB:AE000782; NID:g2689326; PIDN:AAB8979
C;Superfamily: methionyl-tRNA synthetase, dimer-forming
C;Keywords: 11gase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:P42589; GB:AE000389; GB:U00096; NID:g1789451; PIDN:AAC76109.
A;Experimental source: strain K-12, substrain MG1655
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             460 AARRAVASCLQLAKALIIF--AYPVMPESMERMAKAIGLDLENVRLSDAYKVDEVMKLSK 517
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A;Residues: 1-110 <BLAT>
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004
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27.5%; Pred. No. 0.00024;
tive 49; Mismatches 94;
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Pred. No. 1.9e-05;
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Best Local Similarity
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A,Experimental source: strain O157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                 D.J.; Mayhew
K.; Apodaca,
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hypochetical 12.3 kD protein in ileX-ebgR intergenic region - Escherichia coli (strain
C;Species: Escherichia coli
                                                                                                                                                                                     substrain
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                                                                                                      probable tRNA synthetase ygjH [imported] - Escherichia coli (strain O157:H7, C;Species: Bscherichia coli (strain O157:H7, C;Decies: Bscherichia coli (species: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004 C;Accession: C85968 R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, Iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, B.; Potamousis, Nature 409, 529-533, 2001 A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7. A;Reference number: A85480; MUD:21074935; PMID:11206551
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12.6%; Score 198.5; DB 2; Length
Best Local Similarity 41.7%; Pred. No. 1.1e-05;
Matches 43; Conservative 25; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CNLKPAKMRGVLSQAMVMCASSPEKIE-ILAPPNGSVP-GDRI 251
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C;Superfamily: secretion chaperone CsaA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C,Genetics:
A,Gene: ygjH
C,Superfamily: secretion chaperone CsaA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A Status: preliminary
A, Molecule type: DNA
A, Residues: 1-110 <STO>
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Gaps

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RESULT 15
E72297
methionine-tRNA ligase (EC 6.1.1.10) - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Decies: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: E72297
R;Melson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
C,M.
Nature 399, 323-329, 1999
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Status: prealiminary
A;Accession: E72297
A;Status: prealiminary
A;Residues: 1-629 <ARN
A;Residues: 1-629 <ARN
A;Crosa-references: UNIPROT:033925; GB:AE001768; GB:AE000512; NID:g4981619; PIDN:AAD3616
A;Gene: TM1085
C;Gene: TM1085
C;Gene: TM1085
C;Superfamily: methionyl-tRNA synthetase, dimer-forming
C;Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | | | : | | : : : : : : : | | : | | 41 GTVLY-NSLEAVFKVALMTLPVMPDTSEEVFRRVSFEEKPSKEHLENWGVLKPGSTVIHG 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   129 ----KKGEKKEKKQQSIAGSADSKPI---DVSRLDLRIGCIITARKHPDADSLYVEEVDV 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          500 EPLFKKIDAKDFKKVVETVSAEQNAITIDDFSKVDLRIAKVLEAEKVPNSRKLLRIIIDL 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        182 GEIAPRIVVSGLVNHVPLEQMQNRMVILLCNLKPAKMRGVLSQAMVMCASSPEKIEILAP 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Best Local Similarity 26.2%; Pred. No. 0.0005;
Matches 50; Conservative 46; Mismatches 72; Indels 23.
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Search completed: August 3, 2005, 21:58:05
Job time : 42 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          242 PNGSVPGDRIT 252
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Human, differentially regulated protein; prevention; therapy; va
prostate cancer; endothelial monocyte activating polypeptide II;
                                                                                                                                       07-NOV-2002; 2002WO-US035563
Human Pc240 protein.
                                             gene therapy; Pc240
                                                                                           WO2003040331-A2
                                                                     Homo sapiens
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                                                                                                                                                                                                                                                    The invention provides an anti-tumour and anti-angiogenic agent of p43 consisting of two domains, the N-terminal domain (146 amino acids) and C-terminal domain (166 amino acids) containing 11 beta-strands forming a structural core and 3 flanking alpha-helices. p43 is useful as an anti-tumour and anti-angiogenic agent. p43 and its C-terminal cytokine domain (EMAP II) induce regression of fibrosarcoma in immunocompromised mouse while its N-terminal domain does not. p43 is a potent cytokine as determined by the induction of tumour necrosis factor-alpha (TNF-alpha), interleukin-6 (IL-6), IL-8 and matrix metalloprotease-9 or by its polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ELKQELIQAEIQNGVKQIAFPSGTPLHANSMVSENVIQSTAVTTVSSGTKEQIKGGTGDE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VGEIAPRIVVSGLVNHVPLEQMQNRMVILLCNLKPAKMRGVLSQAMVMCASSPEKIEILA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PPNGSVPGDRITFDAFPGEPDKELNPKKKIWEQIQPDLHTNDECVATYKGVPFBVKGKGY 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KKAKEKIEKKGEKKEKKQQSIAGSADSKPIDVSRLDLRIGCIITARKHPDADSLYVEEVD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    180
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                                                                                                                                                                                     Novel anti-tumor and anti-angiogenic agent of p43 comprises N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MANNDAVLKRLEGÇKGAEADQI I EYLKQQVSLLKEKAI LQATLREEKKLRVENAKLKKEI E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MANNDAVLKRLEQKGAEADQIIBYLKQQVSLLKEKAILQATLREEKKLRVENAKLKKEIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KKAKEKI EKKGEKKEKKQOSIAGSADSKPIDVSRLDLRIGCI ITARKHPDADSLYVEEVD
                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                domain and C-terminal domain containing eleven beta-strands forming structural core and three flanking alpha-helices.
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                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 1573; DB 5; Length 312; 100.0%; Pred. No. 1.6e-135;
                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                   Claim 1; Fig 1; 35pp; English.
                                                         14-JUN-2000; 2000WO-KR000630
                                                                                14-JUN-2000; 2000WO-KR000630
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                                                                                                                                                                                                                                                                                                                                                                                                                                  "Best Local Similarity 100.
Matches 312; Conservative
                                                                                                      (IMAG-) IMAGENE CO LTD
                                                                                                                             Ko Y, Kim YS,
                                                                                                                                                   WPI; 2002-098017/13.
N-PSDB; ABA94640.
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 312 AA;
             WO200195927-A1
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                                                                                                                             Kim S,
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AA029575
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AC AA02
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diagnosing, staging, monitoring, prognosticating, preventing, treating or determining the predisposition to diseases or conditions such as prostate cancer. They may be used as molecular markers, drug targets, vaccines, in gene therapy, research, clinical medicine or forensic science. The present sequence is a differentially regulated prostate protein (endothelial monocyte activating polypeptide II), Pc240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to novel differentially regulated genes and polypeptides encoded by them. Sequences of the invention are useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ELKQELIQAEIQNGVKQIAPPSGTPLHANSMVSENVIQSTAVTTVSSGTKEQIKGGTGDE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KKAKEKIEKKGEKGEKGEKKQOSIAGSADSKPIDVSRLDLRIGCIITARKHPDADSLYVBEVD 180
                                                                                                                                                                                                                                                                                                                                                                                New polynucleotide for diagnosing, staging, monitoring, prognosticating, preventing or treating, or determining the predisposition to, diseases ox conditions such as prostate cancer, and for research or forensic science.
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                                                                                                                                                                                                                        Kovace KF,
                                                                                                                                                           (ORIG-) ORIGENE TECHNOLOGIES INC
07-NOV-2001; 2001US-0331041P.
07-NOV-2001; 2001US-0331042P.
18-DEC-2001; 2001US-0340251P.
07-JAN-2002; 2002US-0344791P.
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Matches 312, Conservative
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                                                                                                                                                                                                                                                                                      WPI; 2003-449451/42.
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RESULT 3

AA029575 standard; protein; 312 AA.

(first entry)

27-AUG-2003

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